GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 11, 2005, 08:04:33 ; Search time 218 Seconds
(without alignments)
7873.643 Million cell updates/sec

Title: US-09-896-186C-23
Perfect score: 1049
Sequence: 1 accaaagcattaatttttat.....tttaaccgtccagaaactag 1049

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	111	10.6	5208	3	US-08-781-891-70	Sequence 70, Appl
2	111	10.6	5208	3	US-09-791-211-11	Sequence 11, Appl
3	111	10.6	5208	4	US-09-618-166-70	Sequence 70, Appl
4	111	10.6	5208	4	US-09-949-001-3	Sequence 3, Appli
5	111	10.6	5365	4	US-09-949-001-9	Sequence 9, Appli
6	82.8	7.9	6476	3	US-09-127-670-5	Sequence 5, Appli
7	81.2	7.7	4792	3	US-08-781-891-205	Sequence 205, App
8	81.2	7.7	4792	4	US-09-618-166-205	Sequence 205, App
9	55.4	5.3	98844	3	US-09-791-211-10	Sequence 10, Appl
10	55.4	5.3	143776	4	US-09-949-001-29	Sequence 29, Appl
11	55.4	5.3	144034	4	US-09-949-001-35	Sequence 35, Appl
12	51.2	4.9	29604	3	US-08-781-891-207	Sequence 207, App
13	51.2	4.9	29604	4	US-09-618-166-207	Sequence 207, App
14	49.2	4.7	7218	1	US-08-232-463-14	Sequence 14, Appl
15	45.2	4.3	601	4	US-09-949-001-104	Sequence 104, App
16	45.2	4.3	601	4	US-09-949-001-560	Sequence 560, App
17	42.2	4.0	1141	4	US-09-806-708B-22	Sequence 22, Appl
18	40.8	3.9	13059	4	US-08-956-171E-220	Sequence 220, App
19	40.8	3.9	13059	4	US-08-781-986A-220	Sequence 220, App
20	40	3.8	580073	4	US-08-545-528D-1	Sequence 1, Appli
21	39.2	3.7	1499	3	US-09-300-672-3	Sequence 3, Appli
22	39.2	3.7	1500	3	US-09-300-672-1	Sequence 1, Appli
c 23	38.2	3.6	601	4	US-09-949-016-87979	Sequence 87979, A
c 24	38.2	3.6	670689	4	US-09-949-016-12505	Sequence 12505, A
c 25	38.2	3.6	670690	4	US-09-949-016-14207	Sequence 14207, A
26	38	3.6	601	4	US-09-949-016-27467	Sequence 27467, A
27	38	3.6	601	4	US-09-949-016-27468	Sequence 27468, A
28	38	3.6	601	4	US-09-949-016-68562	Sequence 68562, A
29	38	3.6	601	4	US-09-949-016-68563	Sequence 68563, A
c 30	38	3.6	3595	4	US-09-949-016-492	Sequence 492, App
c 31	38	3.6	24166	4	US-09-949-016-13755	Sequence 13755, A
c 32	38	3.6	91665	4	US-09-949-016-12234	Sequence 12234, A
33	37.2	3.5	5433	3	US-08-929-329-1	Sequence 1, Appli
34	37.2	3.5	767677	4	US-09-949-016-12147	Sequence 12147, A
35	37.2	3.5	767677	4	US-09-949-016-17361	Sequence 17361, A
36	36.6	3.5	256287	4	US-09-949-016-14608	Sequence 14608, A
37	36.6	3.5	294836	4	US-09-949-016-15974	Sequence 15974, A
38	36.2	3.5	5215	4	US-09-231-899-71	Sequence 71, Appl
c 39	36	3.4	99916	4	US-09-816-095-3	Sequence 3, Appli
c 40	35.8	3.4	1653	4	US-09-583-110-2210	Sequence 2210, Ap
c 41	35.8	3.4	1653	4	US-09-107-433-1255	Sequence 1255, Ap
42	35.8	3.4	56976	4	US-09-949-016-17486	Sequence 17486, A
43	35.8	3.4	101674	4	US-09-949-016-12033	Sequence 12033, A
c 44	35.6	3.4	194714	4	US-09-949-016-11869	Sequence 11869, A
c 45	35.6	3.4	196714	4	US-09-949-016-15474	Sequence 15474, A

ALIGNMENTS

RESULT 1
US-08-781-891-70
; Sequence 70, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-781-891-70

Query Match 10.6%; Score 111; DB 3; Length 5208;
Best Local Similarity 54.1%; Pred. No. 1.3e-24;
Matches 272; Conservative 0; Mismatches 225; Indels 6; Gaps 2;

Qy 396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455

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Db        433 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 492

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515

Db        493 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 549

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572

Db        550 AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 609

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632

Db        610 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 669

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692

Db        670 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 729

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752

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Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872

Db        850 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 909

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895

Db        910 TTAGAGATTTTGGATGATACTGT 932


RESULT 2
US-09-791-211-11
; Sequence 11, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 11
;   LENGTH: 5208
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)...(4530)
US-09-791-211-11

  Query Match             10.6%;  Score 111;  DB 3;  Length 5208;
  Best Local Similarity   54.1%;  Pred. No. 1.3e-24;
  Matches  272;  Conservative    0;  Mismatches  225;  Indels    6;  Gaps    2;

Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455

Db        433 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 492

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515

Db        493 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 549

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572

Db        550 AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 609

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632

Db        610 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 669

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692

Db        670 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 729

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752

Db        730 AAAAAGCTGAAATGTACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 789

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812

Db        790 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 849

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872

Db        850 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 909

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895

Db        910 TTAGAGATTTTGGATGATACTGT 932


RESULT 3
US-09-618-166-70
; Sequence 70, Application US/09618166
; Patent No. 6583112
;   GENERAL INFORMATION:
;        APPLICANT: Fu, Ying-Hui
;                   Yu, Chang-En
;                   Oshima, Junko
;                   Mulligan, John T.
;                   Schellenberg, Gerald D.
;        TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                            WERNER'S SYNDROME
;        NUMBER OF SEQUENCES: 209
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed Intellectual Property Law Group
;             STREET: 701 Fifth Avenue, Suite 6300
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/618,166
;             FILING DATE: 17-Jul-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McMasters, David D.
;             REGISTRATION NUMBER: 33,963
;             REFERENCE/DOCKET NUMBER: 240052.419C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 70:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5208 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-09-618-166-70

  Query Match             10.6%;  Score 111;  DB 4;  Length 5208;
  Best Local Similarity   54.1%;  Pred. No. 1.3e-24;
  Matches  272;  Conservative    0;  Mismatches  225;  Indels    6;  Gaps    2;
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Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |    |  ||| |    | | | || || || || || ||||||  ||||
Db        433 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 492

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
              |  |  | |||    ||    || || |||||     | ||| | |||||   |
Db        493 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 549

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | ||| |  |  | ||  ||| |       || | | | || ||  |  |  ||
Db        550 AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 609

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  |||||  |||| | ||||||||  || ||      |||
Db        610 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 669

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
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Db        670 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 729

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |      |    | |  ||| |||||  |   ||   | |    ||  | |
Db        730 AAAAAGCTGAAATGTACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 789

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              ||| ||||||||||    ||   ||| |   | | || |||      | ||||||  |
Db        790 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 849

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || |||||||||||    |    | |||||     |
Db        850 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 909

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||    |   |||| ||||
Db        910 TTAGAGATTTTGGATGATACTGT 932
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RESULT 4
US-09-949-001-3
; Sequence 3, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5208
; TYPE: DNA
; ORGANISM: Human
US-09-949-001-3

Query Match 10.6%; Score 111; DB 4; Length 5208;
Best Local Similarity 54.1%; Pred. No. 1.3e-24;
Matches 272; Conservative 0; Mismatches 225; Indels 6; Gaps 2;

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Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |    |  ||| |    | | | || || || || || ||||||  ||||
Db        433 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 492

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
              |  |  | |||    ||    || || |||||     | ||| | |||||   |
Db        493 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 549

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | ||| |  |  | ||  ||| |       || | | | || ||  |  |  ||
Db        550 AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 609

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  |||||  |||| | ||||||||  || ||      |||
Db        610 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 669

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |   | ||  || ||| ||| |  |||||  | |||||
Db        670 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 729

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |      |    | |  ||| |||||  |   ||   | |    ||  | |
Db        730 AAAAAGCTGAAATGTACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 789

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              ||| ||||||||||    ||   ||| |   | | || |||      | ||||||  |
Db        790 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 849

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || |||||||||||    |    | |||||     |
Db        850 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 909

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||    |   |||| ||||
Db        910 TTAGAGATTTTGGATGATACTGT 932
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RESULT 5
US-09-949-001-9
; Sequence 9, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 5365
; TYPE: DNA
; ORGANISM: Human
US-09-949-001-9

Query Match 10.6%; Score 111; DB 4; Length 5365;
Best Local Similarity 54.1%; Pred. No. 1.3e-24;
Matches 272; Conservative 0; Mismatches 225; Indels 6; Gaps 2;

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Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |    |  ||| |    | | | || || || || || ||||||  ||||
Db        434 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 493

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
              |  |  | |||    ||    || || |||||     | ||| | |||||   |
Db        494 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 550

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | ||| |  |  | ||  ||| |       || | | | || ||  |  |  ||
Db        551 AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 610

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
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Db        611 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 670

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
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Db        671 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 730

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
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Db        731 AAAAAGCTGAAATGCACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 790

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Db        791 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 850

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
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Db        851 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 910

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
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Db        911 TTAGAGATTTTGGATGATACTGT 933


RESULT 6
US-09-127-670-5
; Sequence 5, Application US/09127670
; Patent No. 6228583
; GENERAL INFORMATION:
;  APPLICANT: Massachusetts Institute for Technology
;  APPLICANT: Leonard P. Guarente
;  APPLICANT: David A. Sinclair
;  APPLICANT: David B. Lombard
;  TITLE OF INVENTION: ASSAYS FOR COMPOUNDS WHICH EXTEND LIFE
;  TITLE OF INVENTION: SPAN
;  FILE REFERENCE: MIT-7720pA
;  CURRENT APPLICATION NUMBER: US/09/127,670
;  CURRENT FILING DATE: 1998-07-31
;  EARLIER APPLICATION NUMBER: US 60/054,629
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 6476
;   TYPE: DNA
;   ORGANISM: Murine
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (229)...(4432)
US-09-127-670-5

  Query Match             7.9%;  Score 82.8;  DB 3;  Length 6476;
  Best Local Similarity   53.2%;  Pred. No. 2.1e-15;
  Matches  199;  Conservative    0;  Mismatches  172;  Indels    3;  Gaps    1;

Qy        481 GGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTT 540
              | |  || ||      ||||| | |||||   |   ||  | ||| |  |  | || ||||
Db        494 GCAGAGTCGCAGTGATCCAGTTGTGTGTGTCTGAGAACAAATGTTACTTGTTTCACATTT 553

Qy        541 TT---CATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAA 597
              |      || | | |||| ||  |  |  ||    | | ||| |   | || ||   |
Db        554 CTTCCATGTCAGTTTTCCCCCAGGGATTAAAAATGTTACTAGAAAACAAATCAATTAAGA 613

Qy        598 AGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTA 657
              ||| |||  |||| ||||| || |||     ||| ||| | | ||| | ||  || |
Db        614 AGGCAGGGGTTGGGATTGAAGGGGACCAGTGGAAACTTCTGCGTGATTTTGACGTCAAGT 673

Qy        658 TCAAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAAT 717
              |  |   | ||| ||| ||  | ||| | |||||  |||| |     | |   | |  |
Db        674 TGGAGAGTTTTGTGGAGCTGACGGATGTTGCCAATGAAAAGTTGAAGTGCGCAGAGACCT 733

Qy        718 GGGGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAA 777
              || ||||       ||   | |     |  |  | ||| | ||  ||||    ||    |
Db        734 GGAGCCTCAATGGTCTGGTTAAACACGTCTTAGGGAAACAACTTTTGAAAGACAAGTCCA 793

Qy        778 TCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAA 837
              || |      | || |||     ||  || ||  |  || | |||  ||  || ||||| |
Db        794 TCCGCTGCAGCAATTGGAGTAATTTCCCCCTCACTGAGGACCAGAAACTGTATGCAGCCA 853

Qy        838 CGGATGCTTATGCT 851
              | ||||||||||||
Db        854 CTGATGCTTATGCT 867


RESULT 7
US-08-781-891-205
; Sequence 205, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  205:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4792 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  145..4347
US-08-781-891-205

  Query Match             7.7%;  Score 81.2;  DB 3;  Length 4792;
  Best Local Similarity   52.3%;  Pred. No. 5.5e-15;
  Matches  179;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy        510 GATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCAA 569
              || || || | ||      ||     |  ||     || | | |||| ||  |  |  ||
Db        442 GAGAGCAAATGTTACTTGTTTCACATTTCTTCCATGTCAGTTTTCCCCCAGGGATTAAAA 501

Qy        570 CATCTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTG 629
                  |  | ||| |   | || ||   |||| |||  |||| ||||| || |||     |
Db        502 ATGTTACTAGAAAACAAATCAATTAAGAAGGCAGGGGTTGGGATTGAAGGGGACCAGTGG 561

Qy        630 AAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCC 689
              || ||| | | ||| | ||  || |   |  |   | ||| ||| ||  | ||| | |||
Db        562 AAACTTCTGCGTGATTTTGACGTCAAGTTGGAGAGTTTTGTGGAGCTGACGGATGTTGCC 621

Qy        690 AACCAAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTT 749
              ||  ||||  |     | |   | |  ||| ||||        ||   | |     | |
Db        622 AATGAAAAGTTGAAGTGCGCAGAGACCTGGAGCCTCAATGGTCTGGTTAAACACGTCTTA 681

Qy        750 TGCAAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTG 809
                | ||| | ||  ||||     ||     ||| |      | || |||      ||  || ||
Db        682 GGGAAACAACTTTTGAAAGACAAGTCCATCCGCTGCAGCAATTGGAGTAATTTCCCCCTC 741
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Qy        810 TCAAAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCT 851
              |  || | |||  ||  || ||||| || ||||||||||||
Db        742 ACTGAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCT 783


RESULT 8
US-09-618-166-205
; Sequence 205, Application US/09618166
; Patent No. 6583112
;   GENERAL INFORMATION:
;        APPLICANT: Fu, Ying-Hui
;                   Yu, Chang-En
;                   Oshima, Junko
;                   Mulligan, John T.
;                   Schellenberg, Gerald D.
;        TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                            WERNER'S SYNDROME
;        NUMBER OF SEQUENCES: 209
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed Intellectual Property Law Group
;             STREET: 701 Fifth Avenue, Suite 6300
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/618,166
;             FILING DATE: 17-Jul-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McMasters, David D.
;             REGISTRATION NUMBER: 33,963
;             REFERENCE/DOCKET NUMBER: 240052.419C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 205:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4792 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  145..4347
;        SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-09-618-166-205

  Query Match             7.7%;  Score 81.2;  DB 4;  Length 4792;
  Best Local Similarity   52.3%;  Pred. No. 5.5e-15;
  Matches  179;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy        510 GATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCAA 569
              || || || | ||      ||     |  ||     || | | |||| ||  |  |  ||
Db        442 GAGAGCAAATGTTACTTGTTTCACATTTCTTCCATGTCAGTTTTCCCCCAGGGATTAAAA 501

Qy        570 CATCTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTG 629
              | | ||| |   | || ||   |||| |||  |||| ||||| || |||      |
Db        502 ATGTTACTAGAAAACAAATCAATTAAGAAGGCAGGGGTTGGGATTGAAGGGGACCAGTGG 561

Qy        630 AAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCC 689
              || ||| | | ||| | ||  || |   |  |   | |||  ||| ||  | ||| | |||
Db        562 AAACTTCTGCGTGATTTTGACGTCAAGTTGGAGAGTTTTGTGGAGCTGACGGATGTTGCC 621

Qy        690 AACCAAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTT 749
              ||  ||||  |      | |   | |  ||| ||||       ||   | |      | |
Db        622 AATGAAAAGTTGAAGTGCGCAGAGACCTGGAGCCTCAATGGTCTGGTTAAACACGTCTTA 681

Qy        750 TGCAAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTG 809
              | ||| | ||  ||||    ||    ||| |     | || |||     ||  || ||
Db        682 GGGAAACAACTTTTGAAAGACAAGTCCATCCGCTGCAGCAATTGGAGTAATTTCCCCCTC 741

Qy        810 TCAAAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCT 851
              |  || | |||  ||  || ||||| || ||||||||||||
Db        742 ACTGAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCT 783


RESULT 9
US-09-791-211-10
; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 10
;   LENGTH: 98844
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 24962
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 64383
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 65468
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 65469
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 65470
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 65471
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 87130
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 89049
;   OTHER INFORMATION: unknown
;   OTHER INFORMATION:
US-09-791-211-10

  Query Match             5.3%;  Score 55.4;  DB 3;  Length 98844;
  Best Local Similarity   60.1%;  Pred. No. 9.3e-06;
  Matches   92;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy        545 TTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAGG 604
              | | | | | || ||  |  |  ||     |  ||||| ||  | || ||  ||||| |||
Db      45421 TACAGTTTTTCCCCAGGGATTAAAAATGTTGCTTGAAAATAAAGCAGTTAAAAAGGCAGG 45480

Qy        605 TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA 664
              | | |||||||| || ||      ||| ||| | | ||||| ||   | |   | ||  |
Db      45481 TGTAGGAATTGAAGGAGATCAGTGGAAACTTCTACGTGACTTTGATATCAAATTGAAGAA 45540

Qy        665 TGTTGAGGATCTTTCAGATTTAGCCAACCAAAA 697
              | ||| |||  | ||||| | |||||  ||||
Db      45541 TTTTGTGGAGTTGACAGATGTTGCCAATAAAAA 45573


RESULT 10
US-09-949-001-29
; Sequence 29, Application US/09949001
```

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; Patent No. 6825336
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000789
;  CURRENT APPLICATION NUMBER: US/09/949,001
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/231,323
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 143776
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(143776)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-001-29

  Query Match             5.3%;  Score 55.4;  DB 4;  Length 143776;
  Best Local Similarity   60.1%;  Pred. No. 1.2e-05;
  Matches   92;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy        545 TTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAGG 604
              | | | | | || ||  |  |  ||    |  ||||| ||  | || ||  ||||| |||
Db      33094 TACAGTTTTTCCCCAGGGATTAAAAATGTTGCTTGAAAATAAAGCAGTTAAAAAGGCAGG 33153

Qy        605 TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA 664
              | | ||||||||| || ||       ||| ||| | | ||||| ||   | |   | ||  |
Db      33154 TGTAGGAATTGAAGGAGATCAGTGGAAACTTCTACGTGACTTTGATATCAAATTGAAGAA 33213

Qy        665 TGTTGAGGATCTTTCAGATTTAGCCAACCAAAA 697
              | ||| |||  |  ||||| | |||||  ||||
Db      33214 TTTTGTGGAGTTGACAGATGTTGCCAATAAAAA 33246


RESULT 11
US-09-949-001-35
; Sequence 35, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000789
;  CURRENT APPLICATION NUMBER: US/09/949,001
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/231,323
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 144034
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(144034)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-001-35

  Query Match             5.3%;  Score 55.4;  DB 4;  Length 144034;
  Best Local Similarity   60.1%;  Pred. No. 1.2e-05;
  Matches   92;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy        545 TTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAGG 604
              | | | | | || ||  |  |  ||    |  ||||| ||  | || ||  ||||| |||
Db      33094 TACAGTTTTTCCCCAGGGATTAAAAATGTTGCTTGAAAATAAAGCAGTTAAAAAGGCAGG 33153

Qy        605 TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA 664
              | | ||||||||| || ||       ||| ||| | | ||||| ||   | |   | ||  |
Db      33154 TGTAGGAATTGAAGGAGATCAGTGGAAACTTCTACGTGACTTTGATATCAAATTGAAGAA 33213

Qy        665 TGTTGAGGATCTTTCAGATTTAGCCAACCAAAA 697
              | ||| |||  |  ||||| | |||||  ||||
Db      33214 TTTTGTGGAGTTGACAGATGTTGCCAATAAAAA 33246


RESULT 12
US-08-781-891-207
; Sequence 207, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  207:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29604 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-207

  Query Match             4.9%;  Score 51.2;  DB 3;  Length 29604;
  Best Local Similarity   56.5%;  Pred. No. 9.6e-05;
  Matches   95;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        545 TTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAGG 604
              ||  | | |||| ||  |  |  ||    |  | ||| |   | || ||   |||| |||
Db      19789 TTTAGTTTTCCCCCAGGGATTAAAAATGTTACTAGAAAACAAATCAATTAAGAAGGCAGG 19848

Qy        605 TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA 664
              ||||  ||||| || |||      ||| ||| | | ||| | ||  || |   | |
Db      19849 GGTTGGGATTGAAGGGGACCAGTGGAAACTTCTGCGTGATTTTGACGTCAAGTTGGAGAG 19908

Qy        665 TGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAA 712
              | ||| ||| ||  | ||| | |||||  ||||  | || | |   ||
Db      19909 TTTTGTGGAGCTGACGGATGTTGCCAATGAAAAGGTAGGCGTAATAAA 19956


RESULT 13
US-09-618-166-207
; Sequence 207, Application US/09618166
; Patent No. 6583112
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;   GENERAL INFORMATION:
;        APPLICANT: Fu, Ying-Hui
;                   Yu, Chang-En
;                   Oshima, Junko
;                   Mulligan, John T.
;                   Schellenberg, Gerald D.
;        TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                            WERNER'S SYNDROME
;        NUMBER OF SEQUENCES: 209
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed Intellectual Property Law Group
;             STREET: 701 Fifth Avenue, Suite 6300
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/618,166
;             FILING DATE: 17-Jul-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McMasters, David D.
;             REGISTRATION NUMBER: 33,963
;             REFERENCE/DOCKET NUMBER: 240052.419C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 207:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 29604 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 207:
US-09-618-166-207

  Query Match             4.9%;  Score 51.2;  DB 4;  Length 29604;
  Best Local Similarity   56.5%;  Pred. No. 9.6e-05;
  Matches   95;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        545 TTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAGG 604
              ||  | | |||| ||  |  |  ||     |  | ||| |    | || ||   |||| |||
Db      19789 TTTAGTTTCCCCCAGGGATTAAAAATGTTACTAGAAAACAAATCAATTAAGAAGGCAGG 19848

Qy        605 TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA 664
                |||| ||||| || |||      ||| ||| | | ||| | ||  || |   |  |
Db      19849 GGTTGGGATTGAAGGGGACCAGTGGAAACTTCTGCGTGATTTTGACGTCAAGTTGGAGAG 19908

Qy        665 TGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAA 712
              | ||| ||| ||  | ||| | |||||  ||||  | || | |   ||
Db      19909 TTTTGTGGAGCTGACGGATGTTGCCAATGAAAAGGTAGGCGTAATAAA 19956


RESULT 14
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             4.7%;  Score 49.2;  DB 1;  Length 7218;
  Best Local Similarity   11.5%;  Pred. No. 0.00017;
  Matches   33;  Conservative  140;  Mismatches  113;  Indels    0;  Gaps    0;

Qy          9 ATTAATTTTTATTTTTTTGTTTCAGTAAAAGAAATGTCATCGTCAAATTGGATCGACGAC 68
              | || ||||  ||  ||||    |     | | |  | ||     |  |||| |  | | |
Db        992 ACTATTTTTCCTTCGTTTGCCATACGCTCACAGAATTAATTCCGAGCTTGGCTGCAGGTC 1051

Qy         69 GCTTTTACAGAGGAAGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACAATTTCTCC 128
              |      |    ||    :::::: :: ::  : :: ::    :::::: :  ::::::::
Db       1052 GAGGGAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1111

Qy        129 CGTTCTTCTTCTTCTTCTTCCTCTGCTGCTCCGACCGTACAAGCTACAACCTCCGTCCAT 188
              : :::::::::::::::::::::: :: ::::  :: : :   :: :  ::::: ::: :
Db       1112 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1171

Qy        189 GGCCACGAGGAGGATCCAAATCAAATCCCCAATAATATCCGTCGCCAATTGCCTCGTTCC 248
              :: :     :::   ::   :::::  :  : ::: :: ::  :: :::: ::::
Db       1172 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1231

Qy        249 ATCACTTCTTCTACATCTTATAAACGATTTCCTCTCTCCCGTTGCC 294
               :: :::::::: : :::: :   :  :::::::::::: :: ::
Db       1232 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1277


RESULT 15
US-09-949-001-104
; Sequence 104, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000789
;  CURRENT APPLICATION NUMBER: US/09/949,001
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/231,323
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 848
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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-001-104

  Query Match             4.3%;  Score 45.2;  DB 4;  Length 601;
  Best Local Similarity   58.0%;  Pred. No. 0.00064;
  Matches   80;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy        712 AAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAA 771
              | |  ||| |||||  |   ||   | |    ||  |  | ||| ||||||||||    |
Db        306 AGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGTAAACAGCTCCTGAAAGACA 365

Qy        772 ACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACG 831
              |    ||| |   | | || |||       | ||||||  |  || | |||  ||  || |
Db        366 AGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACTGAGGACCAGAAACTGTATG 425

Qy        832 CAGCAACGGATGCTTATG 849
              |||| || ||||||||||
Db        426 CAGCCACTGATGCTTATG 443


Search completed: July 11, 2005, 09:36:55
Job time : 224 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2005, 08:05:32 ; Search time 49 Seconds
(without alignments)
438.754 Million cell updates/sec

Title: US-09-896-186C-24
Perfect score: 1491
Sequence: 1 MSSSNWIDDAFTEEELLAID.....YASWHLYKVLKDLPDAVSGS 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	352	23.6	1409	4	US-09-949-001-22	Sequence 22, Appl
2	352	23.6	1432	3	US-08-781-891-71	Sequence 71, Appl
3	352	23.6	1432	4	US-09-618-166-71	Sequence 71, Appl
4	352	23.6	1432	4	US-09-949-001-16	Sequence 16, Appl
5	339	22.7	1401	3	US-09-127-670-6	Sequence 6, Appli
6	330	22.1	1401	3	US-08-781-891-206	Sequence 206, App
7	330	22.1	1401	4	US-09-618-166-206	Sequence 206, App
8	175	11.7	186	4	US-09-270-767-32220	Sequence 32220, A
9	169.5	11.4	223	4	US-09-328-352-6289	Sequence 6289, Ap
10	94.5	6.3	858	4	US-09-248-796A-19082	Sequence 19082, A
11	93.5	6.3	661	4	US-09-248-796A-18480	Sequence 18480, A
12	93	6.2	2224	4	US-09-054-272-38	Sequence 38, Appl
13	93	6.2	3079	5	PCT-US94-00198-4	Sequence 4, Appli
14	92.5	6.2	375	4	US-09-270-767-42422	Sequence 42422, A
15	92.5	6.2	481	4	US-09-328-352-4475	Sequence 4475, Ap
16	91.5	6.1	1836	4	US-09-949-016-7432	Sequence 7432, Ap
17	89.5	6.0	260	4	US-09-270-767-33551	Sequence 33551, A
18	89.5	6.0	260	4	US-09-270-767-48768	Sequence 48768, A
19	89	6.0	930	3	US-09-134-001C-5314	Sequence 5314, Ap
20	89	6.0	930	4	US-09-386-962C-10	Sequence 10, Appl
21	87.5	5.9	471	4	US-09-248-796A-14787	Sequence 14787, A
22	87.5	5.9	1375	3	US-09-722-139-2	Sequence 2, Appli
23	87.5	5.9	1375	3	US-09-721-832-2	Sequence 2, Appli
24	87.5	5.9	1375	4	US-09-721-689-2	Sequence 2, Appli
25	86.5	5.8	348	1	US-07-989-845-2	Sequence 2, Appli
26	86.5	5.8	348	5	PCT-US93-11298-2	Sequence 2, Appli
27	86.5	5.8	480	3	US-08-987-367-2	Sequence 2, Appli
28	86.5	5.8	657	4	US-09-284-768A-7	Sequence 7, Appli
29	84.5	5.7	341	4	US-09-800-170-4	Sequence 4, Appli
30	84.5	5.7	480	4	US-09-429-906B-6	Sequence 6, Appli
31	84	5.6	332	4	US-09-252-991A-32235	Sequence 32235, A
32	83	5.6	225	4	US-09-107-532A-5540	Sequence 5540, Ap
33	83	5.6	1516	4	US-09-949-016-6951	Sequence 6951, Ap
34	82.5	5.5	480	3	US-08-987-367-4	Sequence 4, Appli
35	82.5	5.5	608	4	US-09-284-768A-4	Sequence 4, Appli
36	82	5.5	229	4	US-09-198-452A-200	Sequence 200, App
37	82	5.5	231	4	US-09-438-185A-187	Sequence 187, App
38	82	5.5	333	3	US-09-134-001C-4528	Sequence 4528, Ap
39	82	5.5	473	4	US-09-107-532A-5941	Sequence 5941, Ap
40	81.5	5.5	933	4	US-09-248-796A-20513	Sequence 20513, A
41	81	5.4	560	4	US-09-734-237B-66	Sequence 66, Appl
42	81	5.4	561	4	US-09-734-237B-68	Sequence 68, Appl
43	81	5.4	860	4	US-07-945-295-4	Sequence 4, Appli
44	81	5.4	1539	4	US-09-949-016-9653	Sequence 9653, Ap
45	80.5	5.4	381	4	US-09-540-236-3615	Sequence 3615, Ap

ALIGNMENTS

RESULT 1
US-09-949-001-22
; Sequence 22, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1409
; TYPE: PRT
; ORGANISM: Human
US-09-949-001-22

Query Match 23.6%; Score 352; DB 4; Length 1409;
Best Local Similarity 37.7%; Pred. No. 1.5e-29;
Matches 75; Conservative 41; Mismatches 75; Indels 8; Gaps 3;

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Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::    :       |     |    || |:|| | : :| | |
Db         47 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 99

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db        100 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 159

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        160 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 219

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        220 DAYAGFIIYRNLEILDDTV 238
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RESULT 2
US-08-781-891-71
; Sequence 71, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko

```
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1432 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-781-891-71

  Query Match           23.6%;  Score 352;  DB 3;  Length 1432;
  Best Local Similarity  37.7%;  Pred. No. 1.6e-29;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:|| |:: :   |   || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 3
US-09-618-166-71
; Sequence 71, Application US/09618166
; Patent No. 6583112
;   GENERAL INFORMATION:
;        APPLICANT: Fu, Ying-Hui
;                   Yu, Chang-En
;                   Oshima, Junko
;                   Mulligan, John T.
;                   Schellenberg, Gerald D.
;        TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                            WERNER'S SYNDROME
;        NUMBER OF SEQUENCES: 209
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed Intellectual Property Law Group
;             STREET: 701 Fifth Avenue, Suite 6300
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/618,166
;             FILING DATE: 17-Jul-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McMasters, David D.
;             REGISTRATION NUMBER: 33,963
;             REFERENCE/DOCKET NUMBER: 240052.419C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 71:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1432 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-09-618-166-71

  Query Match           23.6%;  Score 352;  DB 4;  Length 1432;
  Best Local Similarity  37.7%;  Pred. No. 1.6e-29;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:|| |:: :   |   || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 4
US-09-949-001-16
; Sequence 16, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000789
;  CURRENT APPLICATION NUMBER: US/09/949,001
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/231,323
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 1432
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-001-16

  Query Match           23.6%;  Score 352;  DB 4;  Length 1432;
  Best Local Similarity  37.7%;  Pred. No. 1.6e-29;
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  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:|| |::    :       |      || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 5
US-09-127-670-6
; Sequence 6, Application US/09127670
; Patent No. 6228583
; GENERAL INFORMATION:
;  APPLICANT: Massachusetts Institute for Technology
;  APPLICANT: Leonard P. Guarente
;  APPLICANT: David A. Sinclair
;  APPLICANT: David B. Lombard
;  TITLE OF INVENTION: ASSAYS FOR COMPOUNDS WHICH EXTEND LIFE
;  TITLE OF INVENTION: SPAN
;  FILE REFERENCE: MIT-7720pA
;  CURRENT APPLICATION NUMBER: US/09/127,670
;  CURRENT FILING DATE: 1998-07-31
;  EARLIER APPLICATION NUMBER: US 60/054,629
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 1401
;   TYPE: PRT
;   ORGANISM: Murine
US-09-127-670-6

  Query Match             22.7%;  Score 339;  DB 3;  Length 1401;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-28;
  Matches   74;  Conservative   42;  Mismatches   72;  Indels   14;  Gaps    5;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              | | : | | |:||  |::       | : :  :  :  :  || |:|| | ::    ||
Db         37 NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG 86

Qy        148 K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG 203
              |   || :|:||  | | : ||    : || |:|:|: :: | |:||:||  ||  |:
Db         87 KRSRVAVIQLCVSENKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD 146

Qy        204 VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY 263
              | ::   :|:|:||:|:   : | |  | : :: |:|||   ||  ||  :||:: |  |
Db        147 VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY 206

Qy        264 AATDAYASWHLYKVLKDLPDAV 285
              |||||||   :|: | :| | |
Db        207 AATDAYAGLIIYQKLGNLGDTV 228


RESULT 6
US-08-781-891-206
; Sequence 206, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  206:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-781-891-206

  Query Match             22.1%;  Score 330;  DB 3;  Length 1401;
  Best Local Similarity   36.0%;  Pred. No. 4.3e-27;
  Matches   72;  Conservative   43;  Mismatches   71;  Indels   14;  Gaps    5;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              | | : | | |:||  |::       | : :  :  :  :  || |:|| | ::    ||
Db         37 NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG 86

Qy        148 K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG 203
              |   || :|:||  : | : ||    : || |: |:|: :: | |:||:||  ||  |:
Db         87 KRSRVAVIQLCVSESKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD 146

Qy        204 VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY 263
              | ::   :|:|:||:|:   : | |  | : :: |:|||   ||  ||  :||:: |  |
Db        147 VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY 206

Qy        264 AATDAYASWHLYKVLKDLPD 283
              |||||||   :|: | :| |
Db        207 AATDAYAGLIIYQKLGNLGD 226


RESULT 7
US-09-618-166-206
; Sequence 206, Application US/09618166
; Patent No. 6583112
;  GENERAL INFORMATION:
;       APPLICANT: Fu, Ying-Hui
;                  Yu, Chang-En
;                  Oshima, Junko
;                  Mulligan, John T.
;                  Schellenberg, Gerald D.
;       TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                           WERNER'S SYNDROME
;       NUMBER OF SEQUENCES: 209
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
```

```
;              STATE: Washington
;              COUNTRY: USA
;              ZIP: 98104-7092
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/618,166
;              FILING DATE: 17-Jul-2000
;              CLASSIFICATION: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: McMasters, David D.
;              REGISTRATION NUMBER: 33,963
;              REFERENCE/DOCKET NUMBER: 240052.419C1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (206) 622-4900
;              TELEFAX: (206) 682-6031
;    INFORMATION FOR SEQ ID NO: 206:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1401 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-618-166-206

  Query Match             22.1%;  Score 330;  DB 4;  Length 1401;
  Best Local Similarity   36.0%;  Pred. No. 4.3e-27;
  Matches   72;  Conservative   43;  Mismatches   71;  Indels   14;  Gaps    5;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              | | : | | |:||  |::       | : :  :  :  :  || |:|| | ::    ||
Db         37 NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG 86

Qy        148 K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG 203
              |   || :|:||  : | : ||    : || |: |:|: :: | |:||:||  ||  |:
Db         87 KRSRVAVIQLCVSESKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD 146

Qy        204 VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY 263
              | ::   :|:|:||:|:   : | |  | : :: |:|||   ||  ||  :||:: |  |
Db        147 VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY 206

Qy        264 AATDAYASWHLYKVLKDLPD 283
              |||||||   :|: | :| |
Db        207 AATDAYAGLIIYQKLGNLGD 226


RESULT 8
US-09-270-767-32220
; Sequence 32220, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32220
;   LENGTH: 186
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-32220

  Query Match             11.7%;  Score 175;  DB 4;  Length 186;
  Best Local Similarity   31.3%;  Pred. No. 3.5e-11;
  Matches   46;  Conservative   22;  Mismatches   71;  Indels    8;  Gaps    3;

Qy        139 SFRKGVLPGKVATVQICVDSNYCDVMHIFH-SGIPQSLQHLIEDSTLVKVGIGIDGDSVK 197
              ||: |  ||| | :|||||   | :  : :   :| :|  ||    :   |: |  |  |

Db          1 SFQTG--PGKSAVIQICVDEKCCYIYQLTNVKKLPAALVALINHPKVRLHGVNIKNDFRK 58

Qy        198 LFHDY-----GVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWE 252
              |  |:         |:  ||    |:      :| |  ||  :  | : |  ::|:  |
Db         59 LARDFPEVTAEPLIEKCVDLGLWCNEVCETGGRWSLERLTNFIAKKAMDKSKKVRMSKWH 118

Qy        253 FYPLSKQQLQYAATDAYASWHLYKVLK 279
                || : || ||| | |    :|: |:
Db        119 VIPLDENQLMYAAIDVYIGQVIYRELE 145


RESULT 9
US-09-328-352-6289
; Sequence 6289, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6289
;   LENGTH: 223
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-6289

  Query Match             11.4%;  Score 169.5;  DB 4;  Length 223;
  Best Local Similarity   27.6%;  Pred. No. 1.9e-10;
  Matches   45;  Conservative   35;  Mismatches   72;  Indels   11;  Gaps    5;

Qy        129 FVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIP--QSLQHLIEDSTLVK 186
              |:| | | :|:|: | :      :|:  :       ::||  :   : || :: :   :|
Db         58 FLGFDSESKPTFQVGEVSTGPHLIQLATEHK----AYLFHVNLSTLKFLQPILSNPKQIK 113

Qy        187 VGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRI 246
              || |:  |   :||  |: ::   ||:       |  :: |:       |: : | |  ::
Db        114 VGFGLKNDK-HIFHKKGIELESCVDLAK-GFSHFGFKQQMGVQKAVALLLGQYLAKSKKV 171

Qy        247 RLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKD---LPDAVS 286
              ||   ||: ||: ||| ||||:  ::  ||    ||  :|
Db        172 GTSNWARKPLTSQQISYAAADAYAALLVFLELKKRKVLPIHIS 214


RESULT 10
US-09-248-796A-19082
; Sequence 19082, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19082
;   LENGTH: 858
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-19082

  Query Match              6.3%;  Score 94.5;  DB 4;  Length 858;
  Best Local Similarity   22.8%;  Pred. No. 0.37;
  Matches   45;  Conservative   32;  Mismatches   93;  Indels   27;  Gaps    8;

Qy         31 SSSSSSSAAPTVQATTSVHGHEEDPNQIPNNI-----RRQLPR--SITSSTSYKRFPLSR 83
```

```
Db        184 SQASVSLLPPTYQAFHSMHEASSADNDSATNITTPQKRKKQKRLESVTSNTGENELKQLA 243

Qy         84 CRARNFPAMRFGGRILY---SKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSF 140

Db        244 LRSSNIPLSELAQKVKQLENDSTTTSVSLEQSKMKENKETQRQLFGMVWLLNSCDLAPT- 302

Qy        141 RKGVLPGK---VATVQICVDSNYCDVMHIFHSGIPQSLQHLIE--DSTLVKVGIGIDGDS 195

Db        303 --AVIPRNRIYARYVQVCADNNLAPVS-------PASFGKLVKILYPNITTRRLGMRGQS 353

Qy        196 VKLFHDYGVSIKDVEDL 212

Db        354 --KYHYCGIKLTGDENM 368


RESULT 11
US-09-248-796A-18480
; Sequence 18480, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18480
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-18480

  Query Match             6.3%;  Score 93.5;  DB 4;  Length 661;
  Best Local Similarity   19.7%;  Pred. No. 0.32;
  Matches   71;  Conservative   44;  Mismatches   98;  Indels  147;  Gaps   14;

Qy          3 SSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSSAAPTVQATTSVHGHEE--------- 53

Db        107 NSNNNNDEDNDIVLLTKD------NFSRSSSGLGSSPGSVKRETSASSMAETSKARKKQK 160

Qy         54 ---DP------------------NQIPNNIRRQLPRSITSSTSYKRFPLSRCRARNFPAM 92

Db        161 SAIDPITGEVNYELILNSLPPNFNDMPYSQRKKLVKSFSESIDYSQFSLF---AKNYLGS 217

Qy         93 RFG-----------------------------------GRILYSKTATEVDKRAMQLIKVL 118

Db       *218 SVGSAKTLKWSSSGTGIASASSSLSRRNRVGSLNTLAGRLL-ARTSTTDFKKLQQAMKP- 275

Qy        119 DTKRDESGIAFVGLDIEWRPSFRKGVLPGKV------ATVQICVD--------------- 157

Db        276 KYNVDEKGAIVLGHEL-----------GKVIGFGAWGTIRECTDQQDGTIRAIKIVKST 323

Qy        158 ----------------SNYCDVMHIFHSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFH 200

Db        324 RDFDGGPGIANHSSGNLNSKTDLTGSMKSKNPRVLEVFKKEIQIWK----------QLHH 373

Qy        201 DYGVSIKDVEDLSD----LANQKIGGD-----KKWGLASLTETLVC---KELLKPNRIRL 248

Db        374 DNILPLIDYYETEDAIFCIMNRINGGTLFEVVDSWGQFNARVNLICGPLEYLFEEQRHRL 433


RESULT 12
US-09-054-272-38
; Sequence 38, Application US/09054272
; Patent No. 6692909
;  GENERAL INFORMATION:
;    APPLICANT:  Lander, Eric S.
;    APPLICANT:  Daley, George Q.
;    APPLICANT:  Cargill, Michele
;    APPLICANT:  Ireland, James S.
;    APPLICANT:  Rozen, Steven G.
;    TITLE OF INVENTION:  CODING SEQUENCE POLYMORPHISMS
;    TITLE OF INVENTION:  IN VASCULAR PATHOLOGY GENES
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/054,272
;      FILING DATE:  01-APR-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI98-05
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  38:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-054-272-38

  Query Match             6.2%;  Score 93;  DB 4;  Length 2224;
  Best Local Similarity   19.2%;  Pred. No. 2.4;
  Matches   58;  Conservative   42;  Mismatches  124;  Indels   78;  Gaps   11;

Qy          4 SNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIR 63

Db        126 ASYLDHTFPAEKM--DDAVAPGREYTYEWSISEDSGPT---------HDDPP--CLTHIY 172

Qy         64 RQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRD 123

Db        173 YSHENLIEDFNSGLIGPLLICKK---------GTLTEGGTQKTFDKQIVLLFAVFDESK- 222

Qy        124 ESGIAFVGLDIEWRPSFR-----KGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHL 178

Db        223 -----------SWSQSSSLMYTVNGYVNGTMPDITVCA-----------HDHISWHLLGM 260

Qy        179 IEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLT------ 232

Db        261 SSGPEL--FSIHFNGQVLEQNHHKVSAITLVSATSTTANMTVGPEGKWIISSLTPKHLQA 318

Qy        233 -------------ETLVCKELLKPNRIRLGNWEFYPLSKQQL-QYAAT------DAYASW 272

Db        319 GMQAYIDIKNCPKKTRNLKKITREQRRHMKRWEYFIAAEEVIWDYAPVIPANMDKKYRSQ 378

Qy        273 HL 274
             ||
Db        379 HL 380
```

```
RESULT 13
PCT-US94-00198-4
; Sequence 4, Application PC/TUS9400198
;  GENERAL INFORMATION:
;    APPLICANT:  Schering Corp.
;    TITLE OF INVENTION:  RAS Associated GAP Proteins
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering Corp.
;      STREET:  1 Girald Farms
;      CITY:  Madison
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  6.0.8
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/00198
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/004,824
;      FILING DATE:  15-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G.
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  DX0352 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201)822-7255
;      TELEFAX:  (201)822-7039
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3079 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Saccharomyces cerevisiae
PCT-US94-00198-4

  Query Match             6.2%;  Score 93;  DB 5;  Length 3079;
  Best Local Similarity   19.3%;  Pred. No. 4.1;
  Matches   57;  Conservative   43;  Mismatches  112;  Indels   84;  Gaps   10;

Qy          9 DAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIRRQLPR 68
              | | :   | ||  :       :   |:       :    :  | :|  ::   : |   |
Db       1976 DDFYKTTFLLIDDVLGQLGQPKMEFSN-------EIPIYIREHMDDYPELYEFMNRHAFR 2028

Qy         69 SITSSTSY----------KRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIK-- 116
              :| :||:|          :  |:      ||         |    ::|  | : ::
Db       2029 NIETSTAYSPSVHESTSSEGIPIITLTMSNF----------SDRHVDIDTVAYKFLQIY 2077

Qy        117 ----------VLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHI 166
                       ::|    : |    |||:    |   |:|| :||  : |:   | :|
Db       2078 ARIWTTKHCLIIDCTEFDEG----GLDMRKFISLVMGLLP-EVAP-KNCIGCYYFNVNET 2131

Qy        167 F---------------HSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVED 211
              |               | ||    :   |  |:|  :|| |  :|:  |  ||: |:
Db       2132 FMDNYGKCLDKDNVYVSSKIPHYFINSNSDEGLMK-SVGITGQGLKVLQDIRVSLHDITL 2190

Qy        212 LSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATD 267
              :  |:                          |  :::|:  |  | :   ||   |
Db       2191 YDEKRNR---------------------FTPVSLKIGDIYFQVLHETPRQYKIRD 2224


RESULT 14
US-09-270-767-42422
; Sequence 42422, Application US/09270767
; Patent No. 6703491
;
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42422
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42422

  Query Match             6.2%;  Score 92.5;  DB 4;  Length 375;
  Best Local Similarity   24.4%;  Pred. No. 0.17;
  Matches   41;  Conservative   24;  Mismatches   48;  Indels   55;  Gaps    8;

Qy         56 NQIPNNIRRQLPRSITSSTSYKR-----------FPLSRCRARNFPAMR----FGGRIL 99
              ||: |: || : |   |: : ||           : | | | |    :|    ||
Db        149 NQLLNSERRTMTRE--SAVATKRNWAILAAGVGLVYVLVRHRHRLLCPLRRVWSFG---- 202

Qy        100 YSKTATEVDKRAMQLIKVL----------DTKRDESGIAFVGLDIEW-------RPSFRK 142
                    : | :| :::|  :          : |         :| | ||        ||
Db        203 -----SLVPQRRIEVINSVQDPTTQWVLNELKNHCQTFKVLGFDCEWITVGGSRRP---- 253

Qy        143 GVLPGKVATVQICVDSNYCDVMHIFH-SGIPQSLQHLIEDSTLVKVGI 189
                  || :|:       | :  : |   ||| |: |:||  ::|||:
Db        254 ------VALLQLSSHRGLCALFRLCHMKQIPQDLRDLLEDDAVIKVGV 295


RESULT 15
US-09-328-352-4475
; Sequence 4475, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4475
;   LENGTH: 481
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-4475

  Query Match             6.2%;  Score 92.5;  DB 4;  Length 481;
  Best Local Similarity   21.5%;  Pred. No. 0.25;
  Matches   46;  Conservative   40;  Mismatches   83;  Indels   45;  Gaps    8;

Qy         63 RRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKR 122
              | : |  : :| :   :||         ||:|  | :: || :       ::| :::  :
Db        142 RHRQPLGVVASITPWNWPLMIAVWHIMPALR-AGNVVISKPSEYTPLSTLRLCEIIQQEV 200

Qy        123 DESGIAFV------GLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQ 176
                 |: |      |  :   |  :| |  |   | |              ||  :|  | |:
Db        201 PAGVISIVVGAGEIGEALSSHPDVQKVVFTGSTRTGQ-----------HIM-AGAAQQLK 248

Qy        177 HLI-----EDSTLVKVGIGIDGDSVKLFH-------DYGVSIKDV-----------EDLS 213
              ||       |: :|     ||  : |:|:           ::| :           : |:
Db        249 HLTLELGGNDAGIVLPDANIDEIADKIFNMAFLNAGQTCAALKRLYVHESQYEALSQKLA 308

Qy        214 DLANQKIGGDKKWGLASLTETLVCKELLKPNRIR 247
              |:|| :: ||   |:|| |     :  :: |:::
Db        309 DIANAQVVGD---GMASSTTFGPVQNQMQYNKVK 339


Search completed: July 11, 2005, 11:55:36
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Job time : 52 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2005, 10:49:54 ; Search time 113 Seconds
(without alignments)
984.633 Million cell updates/sec

Title: US-09-896-186C-24
Perfect score: 1491
Sequence: 1 MSSSNWIDDAFTEEELLAID.....YASWHLYKVLKDLPDAVSGS 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726218 seqs, 386331768 residues

Total number of hits satisfying chosen parameters: 1726218

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1491	100.0	288	10	US-09-896-186B-24	Sequence 24, Appl
2	1439.5	96.5	313	9	US-09-906-226-50	Sequence 50, Appl
3	1439.5	96.5	313	10	US-09-896-186B-2	Sequence 2, Appli
4	676.5	45.4	290	9	US-09-906-226-16	Sequence 16, Appl
5	666.5	44.7	268	15	US-10-424-599-227379	Sequence 227379,
6	411	27.6	256	16	US-10-437-963-118286	Sequence 118286,
7	372.5	25.0	257	16	US-10-425-115-268420	Sequence 268420,
8	352	23.6	1405	16	US-10-741-601-299	Sequence 299, App
9	352	23.6	1405	17	US-10-741-600-847	Sequence 847, App
10	352	23.6	1406	16	US-10-741-601-300	Sequence 300, App
11	352	23.6	1406	17	US-10-741-600-848	Sequence 848, App
12	352	23.6	1432	10	US-09-896-186B-18	Sequence 18, Appl
13	352	23.6	1432	15	US-10-374-077-71	Sequence 71, Appl
14	352	23.6	1432	16	US-10-741-601-302	Sequence 302, App
15	352	23.6	1432	17	US-10-741-600-850	Sequence 850, App
16	352	23.6	1436	16	US-10-741-601-301	Sequence 301, App
17	352	23.6	1436	17	US-10-741-600-849	Sequence 849, App
18	330.5	22.2	643	9	US-09-906-226-49	Sequence 49, Appl
19	330	22.1	1401	15	US-10-374-077-206	Sequence 206, App
20	270	18.1	216	9	US-09-906-226-38	Sequence 38, Appl
21	254	17.0	234	9	US-09-906-226-14	Sequence 14, Appl
22	253.5	17.0	238	15	US-10-424-599-238476	Sequence 238476,
23	249.5	16.7	210	15	US-10-425-114-37706	Sequence 37706, A
24	249.5	16.7	213	9	US-09-906-226-10	Sequence 10, Appl
25	248	16.6	200	16	US-10-425-115-188902	Sequence 188902,
26	245	16.4	236	15	US-10-425-114-71107	Sequence 71107, A
27	238	16.0	197	9	US-09-906-226-12	Sequence 12, Appl
28	238	16.0	201	16	US-10-437-963-143533	Sequence 143533,
29	236.5	15.9	234	9	US-09-906-226-4	Sequence 4, Appli
30	229.5	15.4	210	9	US-09-906-226-40	Sequence 40, Appl
31	229.5	15.4	211	16	US-10-437-963-145011	Sequence 145011,
32	227	15.2	202	16	US-10-425-115-337105	Sequence 337105,
33	227	15.2	210	16	US-10-425-115-337102	Sequence 337102,
34	225.5	15.1	287	16	US-10-437-963-110472	Sequence 110472,
35	218	14.6	201	9	US-09-906-226-2	Sequence 2, Appli
36	218	14.6	204	9	US-09-906-226-24	Sequence 24, Appl
37	218	14.6	204	16	US-10-425-115-247258	Sequence 247258,
38	212	14.2	208	15	US-10-424-599-191095	Sequence 191095,
39	191.5	12.8	571	9	US-09-906-226-42	Sequence 42, Appl
40	188	12.6	159	16	US-10-437-963-150626	Sequence 150626,
41	188	12.6	205	15	US-10-424-599-229443	Sequence 229443,
42	182.5	12.2	621	16	US-10-479-284-18	Sequence 18, Appl
43	181.5	12.2	572	9	US-09-906-226-32	Sequence 32, Appl
44	179.5	12.0	582	9	US-09-906-226-55	Sequence 55, Appl
45	179.5	12.0	582	10	US-09-896-186B-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-896-186B-24
; Sequence 24, Application US/09896186B
; Publication No. US20030166227A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: PB/5-31481A
; CURRENT APPLICATION NUMBER: US/09/896,186B
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-896-186B-24

Query Match 100.0%; Score 1491; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 2e-146;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPN 60
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Db          1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPN 60

Qy         61 NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120
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Qy        121 KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE 180

Qy        181 DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL 240

Qy        241 LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDAVSGS 288
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDAVSGS 288


RESULT 2
US-09-906-226-50
; Sequence 50, Application US/09906226
; Publication No. US20020088026A1
; GENERAL INFORMATION:
;  APPLICANT: Butler, Karla
;  APPLICANT:  Cahoon, Rebecca E.
;  APPLICANT:  Rafalski, Antoni
;  APPLICANT:  Sakai, Hajime
;  TITLE OF INVENTION: Plant RNaseD-Like Genes
;  FILE REFERENCE: BB1467 US NA
;  CURRENT APPLICATION NUMBER: US/09/906,226
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/218993
;  PRIOR FILING DATE: July 17, 2000
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 50
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-09-906-226-50

  Query Match             96.5%;  Score 1439.5;  DB 9;  Length 313;
  Best Local Similarity   95.3%;  Pred. No. 5.4e-141;
  Matches  281;  Conservative    1;  Mismatches    4;  Indels    9;  Gaps    1;

Qy          1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPN 60
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Db          1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPN 60

Qy         61 NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120

Qy        121 KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE 180

Qy        181 DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL 240
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Db        181 DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL 240

Qy        241 LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKV---------LKDLPDAVS 286
              ||||||||||||||||||||||||||||||||||||         | ||   :|
Db        241 LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVTTTKNHLLTLNDLEAKIS 295


RESULT 3
US-09-896-186B-2
; Sequence 2, Application US/09896186B
; Publication No. US20030166227A1
; GENERAL INFORMATION:
;  APPLICANT: Joshua Z. Levin
;  APPLICANT:  Ken Phillips
;  APPLICANT:  Greg Budziszewski
;  APPLICANT:  Fred Meins
;  APPLICANT:  Zhenya Glazov
;  TITLE OF INVENTION: Methods of Controlling Gene Expression
;  FILE REFERENCE: PB/5-31481A
;  CURRENT APPLICATION NUMBER: US/09/896,186B
;  CURRENT FILING DATE:  2002-04-04
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-09-896-186B-2

  Query Match             96.5%;  Score 1439.5;  DB 10;  Length 313;
  Best Local Similarity   95.3%;  Pred. No. 5.4e-141;
  Matches  281;  Conservative    1;  Mismatches    4;  Indels    9;  Gaps    1;

Qy          1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPN 60

Qy         61 NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120

Qy        121 KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE 180

Qy        181 DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL 240

Qy        241 LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKV---------LKDLPDAVS 286
              ||||||||||||||||||||||||||||||||||||         | ||   :|
Db        241 LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVTTTKNHLLTLNDLEAKIS 295


RESULT 4
US-09-906-226-16
; Sequence 16, Application US/09906226
; Publication No. US20020088026A1
; GENERAL INFORMATION:
;  APPLICANT: Butler, Karla
;  APPLICANT:  Cahoon, Rebecca E.
;  APPLICANT:  Rafalski, Antoni
;  APPLICANT:  Sakai, Hajime
;  TITLE OF INVENTION: Plant RNaseD-Like Genes
;  FILE REFERENCE: BB1467 US NA
;  CURRENT APPLICATION NUMBER: US/09/906,226
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/218993
;  PRIOR FILING DATE: July 17, 2000
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
;   LENGTH: 290
;   TYPE: PRT
;   ORGANISM: Glycine max
US-09-906-226-16

  Query Match             45.4%;  Score 676.5;  DB 9;  Length 290;
  Best Local Similarity   49.3%;  Pred. No. 1.6e-61;
  Matches  139;  Conservative   49;  Mismatches   63;  Indels   31;  Gaps    6;

Qy          9 DAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIRRQLPR 68
              :  ||::| ||:|          | |::   |        : |   |       ||:||:
Db         18 EPLTEDDLEAIEA----------SLSNNKKRP-------FNDHTHTP-------RRRLPK 53

Qy         69 SI-----TSSTSYKRFPLSRCRAR-NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKR 122
              |:      :::|:   |   | :|   | |:| |:| ||:|   |:| | :|:::|  |
Db         54 SLIALQHPNASSFSPHP-RPCDSRMTLPVMKFSGQISYSRTFDAVEKAATKLLQILQEKT 112

Qy        123 DESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIEDS 182
              :     :| ||||:|:|||| ||||| :||| |: :| |:|: |||||:|| |:||
Db        113 TDMMQTAIGFDIEWKPTFRKGVPPGKVAVMQICGDTRHCHVLHLIHSGIPQNLQLLLEDP 172
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Qy        183 TLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLK 242
              |::||| |||||:||:| || :|:| | |||  ||||:||| |||||||||| |: |:| |
Db        173 TVLKVGAGIDGDAVKVFRDYNISVKGVTDLSFHANQKLGGDHKWGLASLTEKLLSKQLKK 232

Qy        243 PNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDA 284
              ||:|||||||   |||:||:||||||:||| ||: :||||||
Db        233 PNKIRLGNWEAPVLSKEQLEYAATDAFASWCLYQAIKDLPDA 274


RESULT 5
US-10-424-599-227379
; Sequence 227379, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 227379
;   LENGTH: 268
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_47352C.1.pep
US-10-424-599-227379

  Query Match             44.7%;  Score 666.5;  DB 15;  Length 268;
  Best Local Similarity   51.1%;  Pred. No. 1.6e-60;
  Matches  134;  Conservative   46;  Mismatches   61;  Indels   21;  Gaps    5;

Qy         29 SRSSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIRRQLPRSI-----TSSTSYKRFPLSR 83
              | :| |::   |        : |   |        ||:||:|:      :::|:   |
Db          6 SEASLSNNKKRP-------FNDHTHTP-------RRRLPKSLIALQHPNASSFSPHP-RP 50

Qy         84 CRAR-NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRK 142
              | :|   | |:| |:| ||:|   |:| | :|:::|  |  :     :| ||||:|:||| 
Db         51 CDSRMTLPVMKFSGQISYSRTFDAVEKAATKLLQILQEKTTDMMQTAIGFDIEWKPTFRK 110

Qy        143 GVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDY 202
              || ||||| :||| |: :| |:|: ||||||:|| |:|| |::||| |||||:||:| ||
Db        111 GVPPGKVAVMQICGDTRHCHVLHLIHSGIPQNLQLLLEDPTVLKVGAGIDGDAVKVFRDY 170

Qy        203 GVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQ 262
              :|:| | |||  ||||:||| ||||||||| |: |:| |||:|||||||   |||:||:
Db        171 NISVKGVTDLSFHANQKLGGDHKWGLASLTEKLLSKQLKKPNKIRLGNWEAPVLSKEQLE 230

Qy        263 YAATDAYASWHLYKVLKDLPDA 284
              ||||||:||| ||: :||||||
Db        231 YAATDAFASWCLYQAIKDLPDA 252


RESULT 6
US-10-437-963-118286
; Sequence 118286, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118286
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_21612C.1.pep
US-10-437-963-118286

  Query Match             27.6%;  Score 411;  DB 16;  Length 256;
  Best Local Similarity   37.2%;  Pred. No. 6.2e-34;
  Matches  103;  Conservative   36;  Mismatches   76;  Indels   62;  Gaps    7;

Qy          9 DAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGH-EEDPNQIPNNIRRQLP 67
              ||  | || ||:|  |:    |     |     |  |: | |     |   |
Db         27 DAEAEAELQAIEAAYAAAKRRRLPDWPSPNPVTASASASASGGCSPAPPWAP-------- 78

Qy         68 RSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGI 127
                |  :::      :||  | | | |:| :| ::|:|    ::  ::| :  ||
Db         79 ----SPPAFR----GNVKARYQPVM-FNGSIVYCRTPSKVEKATRDILCKIETMK-ASGQ 128

Qy        128 AFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIEDSTLVKV 187
                :| |:|||  |:                                          |:|
Db        129 VSLGFDLEWRPFPRR-----------------------------------------VQV 146

Qy        188 GIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIG-GDKKWGLASLTETLVCKELLKPNRI 246
              || || |: |:|:|| | :: : |||:||| |:|   |:| |||||| : |:|| ||: |
Db        147 GICIDNDARKMFNDYDVHVQPLMDLSNLANAKLGFPPKRWSLASLTEMVTCRELPKPSNI 206

Qy        247 RLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPD 283
              |:|||| | |||||||||||||| |||||:||: |||
Db        207 RMGNWEAYVLSKQQLQYAATDAYISWHLYEVLQSLPD 243


RESULT 7
US-10-425-115-268420
; Sequence 268420, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 268420
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_1763C.1.pep
US-10-425-115-268420

  Query Match             25.0%;  Score 372.5;  DB 16;  Length 257;
  Best Local Similarity   38.5%;  Pred. No. 6.4e-30;
  Matches   92;  Conservative   41;  Mismatches   81;  Indels   25;  Gaps    8;

Qy          5 NWIDDAFTEEELLAIDAIEASYNFS---RSSSSSSSAAPTVQATTSVHGHEEDPNQIPNN 61
              :| |||  | || | :|  || : |   |     :| :|    : | | |
Db         38 HW-DDA-AEAELQAFEAAYASASASASAKRRRLPDWTSPSP----SPSYHLH---------- 81

Qy         62 IRRQLPRSITSSTSY---KRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVL 118
                | | | |  |: |:       |     |||    : | |:|:| :| || :| |  ::  :
Db         82 -RSQNPVSSGSTPSWTLTPHTPQDNVRARR-QQISFSGKIVYCRTPTEAEKAATDILLKI 139

Qy        119 DTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHL 178
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Db        140 ERMRTPGQVS-LGFDLEWRPFPRRGEPPCKVAVMQLCMEKTLCYVLHIAHSGVPPILKTL 198

Qy        179 IEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVC 237
              :|||: :|||| || |: |: :|| | :: : ||| ||| |:   |:| |||||| : |
Db        199 LEDSSSIKVGICIDNDARKMLNDYNVCVQPLMDLSTLANVKLASPKRWSLASLTEMITC 257


RESULT 8
US-10-741-601-299
; Sequence 299, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 299
;   LENGTH: 1405
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-601-299

  Query Match             23.6%;  Score 352;  DB 16;  Length 1405;
  Best Local Similarity   37.7%;  Pred. No. 1.1e-26;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::    :       |     |    || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 9
US-10-741-600-847
; Sequence 847, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 847
;   LENGTH: 1405
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-847

  Query Match             23.6%;  Score 352;  DB 17;  Length 1405;
  Best Local Similarity   37.7%;  Pred. No. 1.1e-26;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::    :       |     |    || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 10
US-10-741-601-300
; Sequence 300, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 300
;   LENGTH: 1406
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-601-300

  Query Match             23.6%;  Score 352;  DB 16;  Length 1406;
  Best Local Similarity   37.7%;  Pred. No. 1.1e-26;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::    :       |     |    || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 11
US-10-741-600-848
; Sequence 848, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 848
;   LENGTH: 1406
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-848
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  Query Match           23.6%;  Score 352;  DB 17;  Length 1406;
  Best Local Similarity  37.7%;  Pred. No. 1.1e-26;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::   :       |      |    || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 12
US-09-896-186B-18
; Sequence 18, Application US/09896186B
; Publication No. US20030166227A1
; GENERAL INFORMATION:
;  APPLICANT: Joshua Z. Levin
;  APPLICANT:  Ken Phillips
;  APPLICANT:  Greg Budziszewski
;  APPLICANT:  Fred Meins
;  APPLICANT:  Zhenya Glazov
;  TITLE OF INVENTION: Methods of Controlling Gene Expression
;  FILE REFERENCE: PB/5-31481A
;  CURRENT APPLICATION NUMBER: US/09/896,186B
;  CURRENT FILING DATE:  2002-04-04
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 1432
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-896-186B-18

  Query Match           23.6%;  Score 352;  DB 10;  Length 1432;
  Best Local Similarity  37.7%;  Pred. No. 1.1e-26;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::   :       |      |    || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 13
US-10-374-077-71
; Sequence 71, Application US/10374077
; Publication No. US20040006779A1
;   GENERAL INFORMATION:
;        APPLICANT: Fu, Ying-Hui
;                   Yu, Chang-En
;                   Oshima, Junko
;                   Mulligan, John T.
;                   Schellenberg, Gerald D.
;        TITLE OF INVENTION: ANTIBODIES AGAINST GENE PRODUCTS RELATED TO
;                            WERNER'S SYNDROME
;        NUMBER OF SEQUENCES: 209
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed Intellectual Property Law Group
;             STREET: 701 Fifth Avenue, Suite 6300
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/374,077
;             FILING DATE: 25-Feb-2003
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Rosenman, Stephen
;             REGISTRATION NUMBER: 43,058
;             REFERENCE/DOCKET NUMBER: 100107.401D1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 71:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1432 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-374-077-71

  Query Match           23.6%;  Score 352;  DB 15;  Length 1432;
  Best Local Similarity  37.7%;  Pred. No. 1.1e-26;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::   :       |      |    || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 14
US-10-741-601-302
; Sequence 302, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 302
;   LENGTH: 1432
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-601-302

  Query Match             23.6%;  Score 352;  DB 16;  Length 1432;
  Best Local Similarity   37.7%;  Pred. No. 1.1e-26;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::    :       |     |    || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


RESULT 15
US-10-741-600-850
; Sequence 850, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 850
;   LENGTH: 1432
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-850

  Query Match             23.6%;  Score 352;  DB 17;  Length 1432;
  Best Local Similarity   37.7%;  Pred. No. 1.1e-26;
  Matches   75;  Conservative   41;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
              : | : | | |:||  |::    :       |     |    || |:|| | : :| | |
Db         43 DLPFLEFTGSIVYSYDASDCSFLSE------DISMSLSDGDVVGFDMEWPPLYNRGKL-G 95

Qy        148 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
              ||| :|:||  : | : |:    : || |: |:|:  : | |:||:||  ||  |: : :
Db         96 KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL 155

Qy        207 KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
              |:  :|:|:||:|:   : | | || : |: |:|||   ||  ||  :||:: |  ||||
Db        156 KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215

Qy        267 DAYASWHLYKVLKDLPDAV 285
              |||| : :|: |: | | |
Db        216 DAYAGFIIYRNLEILDDTV 234


Search completed: July 11, 2005, 12:05:10
Job time : 115 secs
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                      GenCore version 5.1.6
           Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         July 11, 2005, 08:04:33 ; Search time 5293 Seconds
                                           (without alignments)
                                           1244.278 Million cell updates/sec

Title:          US-09-896-186C-23
Perfect score:  1049
Sequence:       1 accaaagcattaattttat..........tttaaccgtccagaaactag 1049

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters:      12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
                 1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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                 4:  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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                 12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 14:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 15:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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                 17:  /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                 18:  /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
                 19:  /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
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                 21:  /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
                 22:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 23:  /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
                 24:  /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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                 26:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                     %
Result               Query
  No.     Score   Match Length DB  ID                          Description
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     1     1049   100.0   1049  10  US-09-896-186B-23           Sequence 23, Appl
     2      831    79.2    942  10  US-09-896-186B-1            Sequence 1, Appli
     3    276.2    26.3   1170  9  US-09-906-226-15            Sequence 15, Appl
     4    276.2    26.3   1253  18  US-10-424-599-84537         Sequence 84537, A
     5    112.2    10.7   5765  19  US-10-741-601-18            Sequence 18, Appl
     6    112.2    10.7   5765  21  US-10-741-600-22            Sequence 22, Appl
     7    112.2    10.7   6428  19  US-10-741-601-15            Sequence 15, Appl
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       8    112.2    10.7    6428  21  US-10-741-600-19          Sequence 19, Appl
       9    112.2    10.7    6431  19  US-10-741-601-16          Sequence 16, Appl
      10    112.2    10.7    6431  21  US-10-741-600-20          Sequence 20, Appl
      11    112.2    10.7    6521  19  US-10-741-601-17          Sequence 17, Appl
      12    112.2    10.7    6521  21  US-10-741-600-21          Sequence 21, Appl
      13      111    10.6    4299  10  US-09-896-186B-17         Sequence 17, Appl
      14      111    10.6    5189  9  US-09-954-456-1131        Sequence 1131, Ap
      15      111    10.6    5189  9  US-09-292-758-31          Sequence 31, Appl
      16      111    10.6    5189  21  US-10-843-641A-4158       Sequence 4158, Ap
      17      111    10.6    5208  17  US-10-374-077-70          Sequence 70, Appl
      18      111    10.6    5208  21  US-10-467-182-11          Sequence 11, Appl
      19    109.8    10.5     800  20  US-10-425-115-83757       Sequence 83757, A
      20    105.8    10.1     824  19  US-10-437-963-15803       Sequence 15803, A
      21     95.6     9.1     724  18  US-10-424-599-86601       Sequence 86601, A
      22     81.2     7.7    4792  17  US-10-374-077-205         Sequence 205, App
      23       56     5.3    1047  9  US-09-906-226-37          Sequence 37, Appl
      24     55.4     5.3     201  19  US-10-741-601-806         Sequence 806, App
      25     55.4     5.3     201  19  US-10-741-601-822         Sequence 822, App
      26     55.4     5.3     201  19  US-10-741-601-838         Sequence 838, App
      27     55.4     5.3     201  19  US-10-741-601-859         Sequence 859, App
      28     55.4     5.3     201  21  US-10-741-600-2988        Sequence 2988, Ap
      29     55.4     5.3     201  21  US-10-741-600-3004        Sequence 3004, Ap
      30     55.4     5.3     201  21  US-10-741-600-3020        Sequence 3020, Ap
      31     55.4     5.3     201  21  US-10-741-600-3043        Sequence 3043, Ap
      32     55.4     5.3   98844  21  US-10-467-182-10          Sequence 10, Appl
      33     55.4     5.3  151870  19  US-10-741-601-5614        Sequence 5614, Ap
      34     55.4     5.3  151870  21  US-10-741-600-17561       Sequence 17561, A
      35     51.2     4.9     610  18  US-10-424-599-76746       Sequence 76746, A
      36     51.2     4.9   29604  17  US-10-374-077-207         Sequence 207, App
      37     44.4     4.2     449  18  US-10-276-774-284         Sequence 284, App
      38     44.4     4.2    2303  19  US-10-479-284-50          Sequence 50, Appl
      39     44.4     4.2    3149  9  US-09-729-674-127         Sequence 127, App
      40     44.4     4.2    3149  21  US-10-913-553-127         Sequence 127, App
c     41     42.8     4.1     408  21  US-10-275-323A-13         Sequence 13, Appl
c     42     41.4     3.9     941  14  US-10-123-155-464         Sequence 464, App
c     43     41.4     3.9     941  15  US-10-146-731-464         Sequence 464, App
c     44     41.4     3.9     941  15  US-10-140-472-464         Sequence 464, App
c     45     41.4     3.9     941  15  US-10-141-761-464         Sequence 464, App

                                  ALIGNMENTS


RESULT 1
US-09-896-186B-23
; Sequence 23, Application US/09896186B
; Publication No. US20030166227A1
; GENERAL INFORMATION:
;  APPLICANT: Joshua Z. Levin
;  APPLICANT:  Ken Phillips
;  APPLICANT:  Greg Budziszewski
;  APPLICANT:  Fred Meins
;  APPLICANT:  Zhenya Glazov
;  TITLE OF INVENTION: Methods of Controlling Gene Expression
;  FILE REFERENCE: PB/5-31481A
;  CURRENT APPLICATION NUMBER: US/09/896,186B
;  CURRENT FILING DATE:  2002-04-04
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 1049
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-896-186B-23

  Query Match             100.0%;  Score 1049;  DB 10;  Length 1049;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-290;
  Matches 1049;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACCAAAGCATTAATTTTTATTTTTTTGTTTCAGTAAAAGAAATGTCATCGTCAAATTGGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCAAAGCATTAATTTTTATTTTTTTGTTTCAGTAAAAGAAATGTCATCGTCAAATTGGA 60
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Qy         61 TCGACGACGCTTTTACAGAGGAAGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGACGACGCTTTTACAGAGGAAGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACA 120

Qy        121 ATTTCTCCCGTTCTTCTTCTTCTTCTTCCTCTGCTGCTCCGACCGTACAAGCTACAACCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTTCTCCCGTTCTTCTTCTTCTTCTTCCTCTGCTGCTCCGACCGTACAAGCTACAACCT 180

Qy        181 CCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCAATAATATCCGTCGCCAATTGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCAATAATATCCGTCGCCAATTGC 240

Qy        241 CTCGTTCCATCACTTCTTCTACATCTTATAAACGATTTCCTCTCTCCCGTTGCCGAGCTA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCGTTCCATCACTTCTTCTACATCTTATAAACGATTTCCTCTCTCCCGTTGCCGAGCTA 300

Qy        301 GGAATTTTCCAGCAATGAGGTTTGGTGGTAGGATTTTGTATAGCAAGACTGCTACTGAGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAATTTTCCAGCAATGAGGTTTGGTGGTAGGATTTTGTATAGCAAGACTGCTACTGAGG 360

Qy        361 TTGATAAGCGAGCAATGCAGCTTATTAAAGTTCTTGATACCAAGAGAGATGAATCTGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTGATAAGCGAGCAATGCAGCTTATTAAAGTTCTTGATACCAAGAGAGATGAATCTGGAA 420

Qy        421 TAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCGG 480

Qy        481 GGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTT 540

Qy        541 TTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGG 600

Qy        601 TAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCA 660

Qy        661 AAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGGG 720

Qy        721 GCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAATCA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAATCA 780

Qy        781 GGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACGG 840

Qy        841 ATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGCTGTCAGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGCTGTCAGTG 900

Qy        901 GCTCATAACGTGAAGGAGGAAGCTTAAAGGTTAGCCTATAACCCCAAGAGTTAGCATCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCTCATAACGTGAAGGAGGAAGCTTAAAGGTTAGCCTATAACCCCAAGAGTTAGCATCAA 960

Qy        961 ATGATATGATACACCTAATCTAGTCAAGTAGATGCAATTCTTGTGAATATTGTATCTAGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATGATATGATACACCTAATCTAGTCAAGTAGATGCAATTCTTGTGAATATTGTATCTAGT 1020

Qy       1021 TCTGGTCCCTTTAACCGTCCAGAAACTAG 1049
              |||||||||||||||||||||||||||||
Db       1021 TCTGGTCCCTTTAACCGTCCAGAAACTAG 1049
```

RESULT 2
US-09-896-186B-1
; Sequence 1, Application US/09896186B
; Publication No. US20030166227A1

; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: PB/5-31481A
; CURRENT APPLICATION NUMBER: US/09/896,186B
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-896-186B-1

Query Match 79.2%; Score 831; DB 10; Length 942;
Best Local Similarity 96.1%; Pred. No. 1.3e-227;
Matches 852; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Qy         42 ATGTCATCGTCAAATTGGATCGACGACGCTTTTACAGAGGAAGAGCTTCTCGCTATCGAC 101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCATCGTCAAATTGGATCGACGACGCTTTTACAGAGGAAGAGCTTCTCGCTATCGAC 60

Qy        102 GCCATCGAAGCTTCCTACAATTTCTCCCGTTCTTCTTCTTCTTCTTCCTCTGCTGCTCCG 161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCGAAGCTTCCTACAATTTCTCCCGTTCTTCTTCTTCTTCTTCCTCTGCTGCTCCG 120

Qy        162 ACCGTACAAGCTACAACCTCCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCAAT 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCGTACAAGCTACAACCTCCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCAAT 180

Qy        222 AATATCCGTCGCCAATTGCCTCGTTCCATCACTTCTTCTACATCTTATAAACGATTTCCT 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATATCCGTCGCCAATTGCCTCGTTCCATCACTTCTTCTACATCTTATAAACGATTTCCT 240

Qy        282 CTCTCCCGTTGCCGAGCTAGGAATTTTCCAGCAATGAGGTTTGGTGGTAGGATTTTGTAT 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCTCCCGTTGCCGAGCTAGGAATTTTCCAGCAATGAGGTTTGGTGGTAGGATTTTGTAT 300

Qy        342 AGCAAGACTGCTACTGAGGTTGATAAGCGAGCAATGCAGCTTATTAAAGTTCTTGATACC 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCAAGACTGCTACTGAGGTTGATAAGCGAGCAATGCAGCTTATTAAAGTTCTTGATACC 360

Qy        402 AAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTT 461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTT 420

Qy        462 AGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTAT 521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTAT 480

Qy        522 TGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAA 581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAA 540

Qy        582 GATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCAT 641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCAT 600

Qy        642 GACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATT 701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATT 660

Qy        702 GGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTC 761
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTC 720

Qy        762 CTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAG 821
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAG 780
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Qy        822 TTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGAC 881
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    |
Db        781 TTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTAACAACAACG 840

Qy        882 CTTCCTGATGCTGTCAGTGGCTCATAACGTGAAGGAGGAAGCTTAAA 928
                  ||  | |||    |    | | ||||| |  || || | |
Db        841 AAAAACCATCTTCTCACACTCAACGACCTTGAAGCAAAAATCTCACA 887


RESULT 3
US-09-906-226-15
; Sequence 15, Application US/09906226
; Publication No. US20020088026A1
; GENERAL INFORMATION:
;  APPLICANT: Butler, Karla
;  APPLICANT:  Cahoon, Rebecca E.
;  APPLICANT:  Rafalski, Antoni
;  APPLICANT:  Sakai, Hajime
;  TITLE OF INVENTION: Plant RNaseD-Like Genes
;  FILE REFERENCE: BB1467 US NA
;  CURRENT APPLICATION NUMBER: US/09/906,226
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/218993
;  PRIOR FILING DATE: July 17, 2000
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
;   LENGTH: 1170
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-906-226-15

  Query Match             26.3%;  Score 276.2;  DB 9;  Length 1170;
  Best Local Similarity   66.6%;  Pred. No. 3.4e-68;
  Matches  395;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy        300 AGGAATTTTCCAGCAATGAGGTTTGGTGGTAGGATTTTGTATAGCAAGACTGCTACTGAG 359
              | ||  || || | ||||| |||| |||||   ||||  ||||||| ||||  |  ||
Db        229 ATGACATTGCCTGTAATGAAGTTTAGTGGTCAAATTTCTTATAGCAGGACTTTTGATGCT 288

Qy        360 GTTGATAAGCGAGCAATGCAGCTTATTAAAGTTCTTGATACCAAGAGAGATGAATCTGGA 419
              || || ||    ||||   ||||  |  || ||||  |    || |     ||
Db        289 GTAGAGAAAGCTGCAACAAAGCTCTTACAAATTCTCCAAGAAAAAACGACCGACATGATG 348

Qy        420 ATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCG 479
              | ||    |||| || || |||||||||| ||| |  || ||||||||||||  ||
Db        349 CAAACTGCAATTGGATTTGACATTGAGTGGAAACCCACCTTCAGAAAAGGTGTTCCTCCC 408

Qy        480 GGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATT 539
              || ||||| ||      | |||||||||| || | ||   ||||| ||||| | ||| |
Db        409 GGAAAGGTAGCAGTGATGCAGATATGTGGTGACACTAGACATTGTCATGTTCTACATCTA 468

Qy        540 TTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAG 599
              |||||||||| |||||||||  | | || | | |  |||||||| | ||| |  | |||
Db        469 ATTCATTCTGGAATCCCTCAAAATTTACAGCTTTGCTTGAAGATCCCACAGTCTTGAAG 528

Qy        600 GTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATC 659
              || ||   ||| |||||||||||  |||||||| ||||     || |||     |  | |
Db        529 GTTGGAGCTGGGATTGATGGTGATGCTGTGAAGGTTTTTAGAGATTATAACATATCTGTT 588

Qy        660 AAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGG 719
              |||| |||   |||||||||     |   || || |||||  |||||||||| | || |||
Db        589 AAAGGTGTGACGGATCTTTCTTTTCATGCTAATCAAAAGCTTGGTGGAGATCATAAGTGG 648

Qy        720 GGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAATC 779
              || ||||| ||  | ||||| | |||| | |  ||| |||| |||||| |||| |||
Db        649 GGTCTTGCATCTTTGACTGAAAAACTTCTATCAAAACAGCTTAAAAAGCCCAACAAAATA 708

Qy        780 AGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACG 839
              || || || |||||  |  |  | |||||||| |||| || | || || |||||
Db        709 AGACTGGGAAATTGGGAGGCTCCTGTTTTGTCAAAGGAGCAACTAGAGTATGCTGCAACA 768

Qy        840 GATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGC 892
              ||||||| |||||| |||  |||||| |||   |||| || || || || ||
Db        769 GATGCTTTTGCTTCTTGGTGTCTTTATCAGGCGATTAAAGATCTCCCGGACGC 821


RESULT 4
US-10-424-599-84537
; Sequence 84537, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 84537
;   LENGTH: 1253
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_47352C.1
US-10-424-599-84537

  Query Match             26.3%;  Score 276.2;  DB 18;  Length 1253;
  Best Local Similarity   66.6%;  Pred. No. 3.6e-68;
  Matches  395;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy        300 AGGAATTTTCCAGCAATGAGGTTTGGTGGTAGGATTTTGTATAGCAAGACTGCTACTGAG 359
              | ||  || || | ||||| |||| |||||   ||||  ||||||| ||||  |  ||
Db        276 ATGACATTGCCTGTAATGAAGTTTAGTGGTCAAATTTCTTATAGCAGGACTTTTGATGCT 335

Qy        360 GTTGATAAGCGAGCAATGCAGCTTATTAAAGTTCTTGATACCAAGAGAGATGAATCTGGA 419
              || || ||    ||||   ||||  |  || ||||  |    || |     ||
Db        336 GTAGAGAAAGCTGCAACAAAGCTCTTACAAATTCTCCAAGAAAAAACGACCGACATGATG 395

Qy        420 ATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCG 479
              | ||    |||| || || |||||||||| ||| |  || ||||||||||||  ||
Db        396 CAAACTGCAATTGGATTTGACATTGAGTGGAAACCCACCTTCAGAAAAGGTGTTCCTCCC 455

Qy        480 GGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATT 539
              || ||||| ||      | |||||||||| || | ||   ||||| ||||| | ||| |
Db        456 GGAAAGGTAGCAGTGATGCAGATATGTGGTGACACTAGACATTGTCATGTTCTACATCTA 515

Qy        540 TTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAG 599
              |||||||||| |||||||||| | | || | | |  |||||||| | ||| |  | |||
Db        516 ATTCATTCTGGAATCCCTCAAAATTTACAGCTTTTGCTTGAAGATCCCACAGTCTTGAAG 575

Qy        600 GTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATC 659
              || ||   ||| |||||||||||  |||||||| ||||     || |||     |  | |
Db        576 GTTGGAGCTGGGATTGATGGTGATGCTGTGAAGGTTTTTAGAGATTATAACATATCTGTT 635

Qy        660 AAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGG 719
              |||| |||   |||||||||     |   || || |||||  |||||||||| | || |||
Db        636 AAAGGTGTGACGGATCTTTCTTTTCATGCTAATCAAAAGCTTGGTGGAGATCATAAGTGG 695

Qy        720 GGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAATC 779
              || ||||| ||  | ||||| | |||| | |  ||| |||| |||||| |||| |||
Db        696 GGTCTTGCATCTTTGACTGAAAAACTTCTATCAAAACAGCTTAAAAAGCCCAACAAAATA 755

Qy        780 AGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACG 839
              || || || |||||  |  |  | |||||||| |||| || | || || |||||
Db        756 AGACTGGGAAATTGGGAGGCTCCTGTTTTGTCAAAGGAGCAACTAGAGTATGCTGCAACA 815

Qy        840 GATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGC 892
              ||||||| |||||| |||  |||||| |||   |||| || || || || ||
Db        816 GATGCTTTTGCTTCTTGGTGTCTTTATCAGGCGATTAAAGATCTCCCGGACGC 868
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RESULT 5
US-10-741-601-18
; Sequence 18, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 5765
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-18

  Query Match             10.7%;  Score 112.2;  DB 19;  Length 5765;
  Best Local Similarity   54.1%;  Pred. No. 1.1e-20;
  Matches  272;  Conservative    1;  Mismatches  224;  Indels    6;  Gaps    2;

Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |     |  ||| |     | | | || || || || || |||||  ||||
Db        990 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 1049

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
                | |  | |||    ||    || || |||||     | ||| | |||||   |
Db       1050 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 1106

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |  | ||| |  |  | || :||| |      || | | | || ||  |  |  ||
Db       1107 AGCAAATGTTACTTGTTCCACRTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 1166

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  ||||| |||| | |||||||| || ||       |||
Db       1167 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 1226

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |   | ||  || ||| ||  |  ||||| | |||||
Db       1227 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 1286

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |      |  | |||  |||||  |   ||   | |   ||  | |
Db       1287 AAAAAGCTGAAATGYACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 1346

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              |||  ||||||||||    ||     ||| |   | | || |||       | ||||||  |
Db       1347 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 1406

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db       1407 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 1466

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||     |   |||| ||||
Db       1467 TTAGAGATTTTGGATGATACTGT 1489


RESULT 6
US-10-741-600-22
; Sequence 22, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 5765
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-22

  Query Match             10.7%;  Score 112.2;  DB 21;  Length 5765;
  Best Local Similarity   54.1%;  Pred. No. 1.1e-20;
  Matches  272;  Conservative    1;  Mismatches  224;  Indels    6;  Gaps    2;

Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |     |  ||| |     | | | || || || || || |||||  ||||
Db        990 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 1049

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
                | |  | |||    ||    || || |||||     | ||| | |||||   |
Db       1050 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 1106

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |  | ||| |  |  | || :||| |      || | | | || ||  |  |  ||
Db       1107 AGCAAATGTTACTTGTTCCACRTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 1166

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  ||||| |||| | |||||||| || ||       |||
Db       1167 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 1226

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |   | ||  || ||| ||  |  ||||| | |||||
Db       1227 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 1286

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |      |  | |||  |||||  |   ||   | |   ||  | |
Db       1287 AAAAAGCTGAAATGYACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 1346

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              |||  ||||||||||    ||     ||| |   | | || |||       | ||||||  |
Db       1347 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 1406

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db       1407 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 1466

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||     |   |||| ||||
Db       1467 TTAGAGATTTTGGATGATACTGT 1489


RESULT 7
US-10-741-601-15
; Sequence 15, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 6428
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-15

  Query Match             10.7%;  Score 112.2;  DB 19;  Length 6428;
  Best Local Similarity   54.1%;  Pred. No. 1.2e-20;
  Matches  272;  Conservative    1;  Mismatches  224;  Indels    6;  Gaps    2;

Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |     |  ||| |     | | | || || || || || |||||  ||||
Db        990 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 1049
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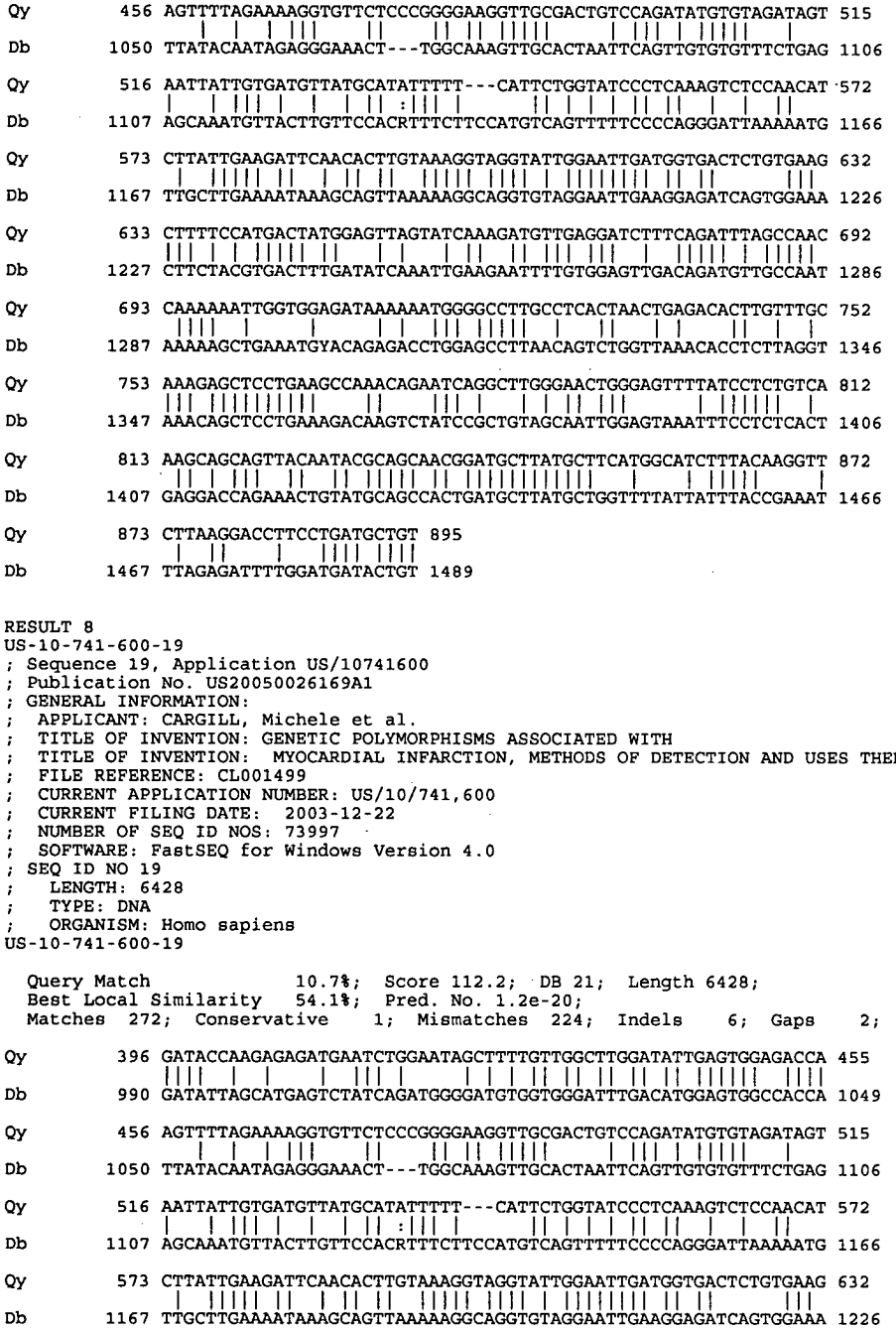
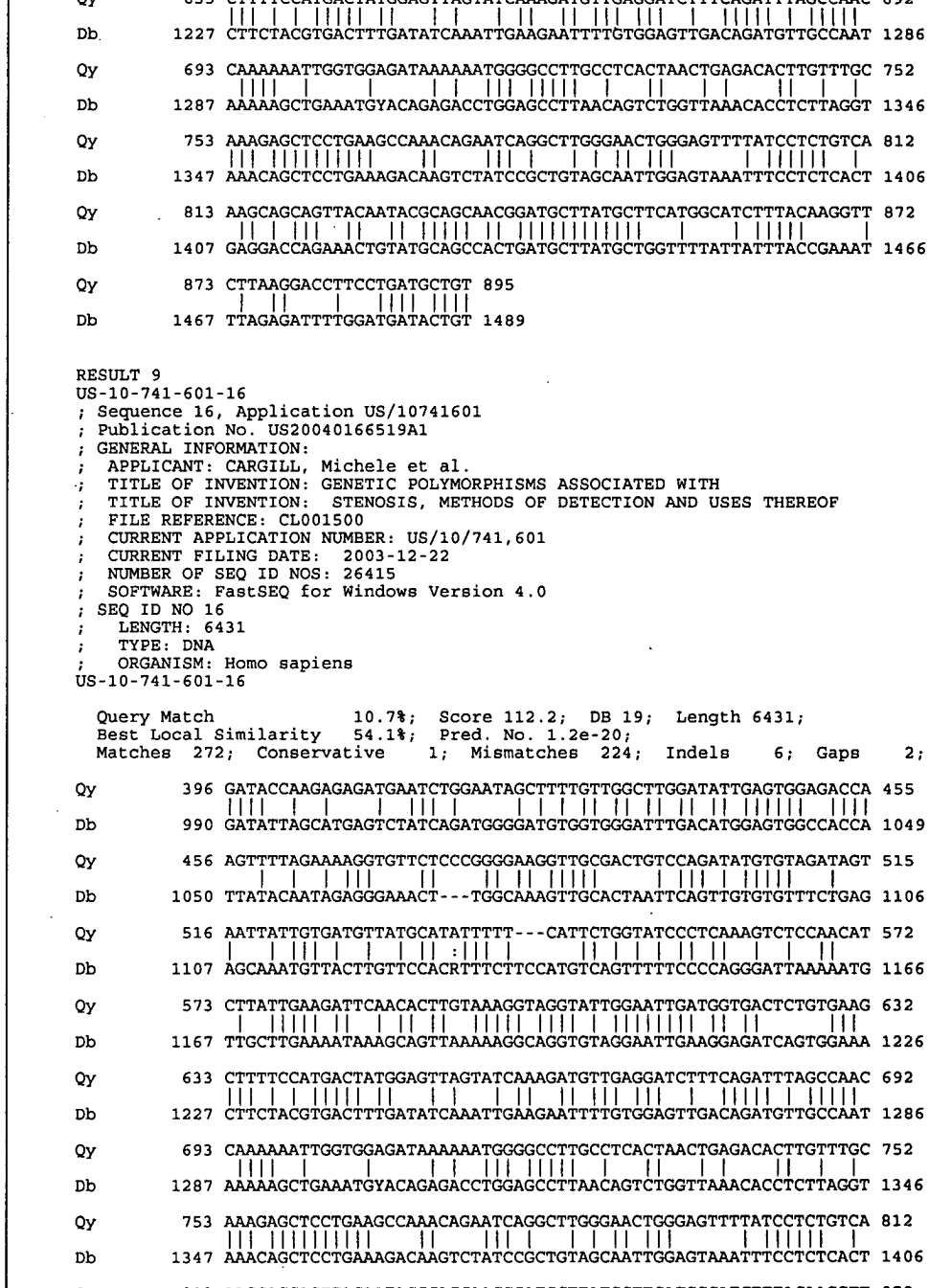


RESULT 8
US-10-741-600-19
; Sequence 19, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 6428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-19

Query Match 10.7%; Score 112.2; DB 21; Length 6428;
Best Local Similarity 54.1%; Pred. No. 1.2e-20;
Matches 272; Conservative 1; Mismatches 224; Indels 6; Gaps 2;



RESULT 9
US-10-741-601-16
; Sequence 16, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6431
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-16

Query Match 10.7%; Score 112.2; DB 19; Length 6431;
Best Local Similarity 54.1%; Pred. No. 1.2e-20;
Matches 272; Conservative 1; Mismatches 224; Indels 6; Gaps 2;

```
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db       1407 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 1466

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||    |   |||| ||||
Db       1467 TTAGAGATTTTGGATGATACTGT 1489


RESULT 10
US-10-741-600-20
; Sequence 20, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 6431
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20

  Query Match            10.7%;  Score 112.2;  DB 21;  Length 6431;
  Best Local Similarity   54.1%;  Pred. No. 1.2e-20;
  Matches  272;  Conservative    1;  Mismatches  224;  Indels    6;  Gaps    2;

Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |    |  ||| |     | | | || || || || || |||||  ||||
Db        990 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 1049

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
                |  | | |||    ||    || || |||||     | ||| | |||||   |
Db       1050 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 1106

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | ||| |  |  | || :||| |      || | | | || ||  |  |  ||
Db       1107 AGCAAATGTTACTTGTTCCACRTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 1166

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  ||||| |||| | |||||||| || ||      |||
Db       1167 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 1226

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |    | ||  || ||| |||  |  |||||  | |||||
Db       1227 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 1286

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |      |   | |  ||| |||||  |    ||   | |    ||  | |
Db       1287 AAAAAGCTGAAATGYACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 1346

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              ||| ||||||||||    ||   ||| |   | | || |||      | ||||||  |
Db       1347 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 1406

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db       1407 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 1466

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||    |   |||| ||||
Db       1467 TTAGAGATTTTGGATGATACTGT 1489


RESULT 11
US-10-741-601-17
; Sequence 17, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 6521
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-17

  Query Match            10.7%;  Score 112.2;  DB 19;  Length 6521;
  Best Local Similarity   54.1%;  Pred. No. 1.2e-20;
  Matches  272;  Conservative    1;  Mismatches  224;  Indels    6;  Gaps    2;

Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |    |  ||| |     | | | || || || || || |||||  ||||
Db        990 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 1049

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
                |  | | |||    ||    || || |||||     | ||| | |||||   |
Db       1050 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 1106

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | ||| |  |  | || :||| |      || | | | || ||  |  |  ||
Db       1107 AGCAAATGTTACTTGTTCCACRTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 1166

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  ||||| |||| | |||||||| || ||      |||
Db       1167 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 1226

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |    | ||  || ||| |||  |  |||||  | |||||
Db       1227 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 1286

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |      |   | |  ||| |||||  |    ||   | |    ||  | |
Db       1287 AAAAAGCTGAAATGYACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 1346

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              ||| ||||||||||    ||   ||| |   | | || |||      | ||||||  |
Db       1347 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 1406

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db       1407 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 1466

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||    |   |||| ||||
Db       1467 TTAGAGATTTTGGATGATACTGT 1489


RESULT 12
US-10-741-600-21
; Sequence 21, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 6521
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-21
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Query Match 10.7%; Score 112.2; DB 21; Length 6521;
Best Local Similarity 54.1%; Pred. No. 1.2e-20;
Matches 272; Conservative 1; Mismatches 224; Indels 6; Gaps 2;

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Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |    | ||| |     | | | || || || || || ||||||  ||||
Db        990 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 1049

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
                |  |  | |||    ||    || || |||||     | ||| | |||||   |
Db       1050 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 1106

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | |||  |   |  || :||| |      || | |  | ||  ||   |  | ||
Db       1107 AGCAAATGTTACTTGTTCCACRTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 1166

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  ||||| |||| | |||||||| || ||       |||
Db       1167 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 1226

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |   | ||  || ||| |||  |  |||||  | |||||
Db       1227 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 1286

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |     |     | |  ||| |||||  |   ||   | |    ||  |  |
Db       1287 AAAAAGCTGAAATGYACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 1346

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              ||| ||||||||||     ||    ||| |   | | || |||       | ||||||  |
Db       1347 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 1406

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db       1407 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 1466

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||     |   |||| ||||
Db       1467 TTAGAGATTTTGGATGATACTGT 1489
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RESULT 13
US-09-896-186B-17
; Sequence 17, Application US/09896186B
; Publication No. US20030166227A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: PB/5-31481A
; CURRENT APPLICATION NUMBER: US/09/896,186B
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 4299
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-896-186B-17

Query Match 10.6%; Score 111; DB 10; Length 4299;
Best Local Similarity 54.1%; Pred. No. 2.1e-20;
Matches 272; Conservative 0; Mismatches 225; Indels 6; Gaps 2;

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Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |    | ||| |     | | | || || || || || ||||||  ||||
Db        202 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 261

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
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Db        262 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 318

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | |||  |   |  || :||| |      || | |  | ||  ||   |  | ||
Db        319 AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 378

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  ||||| |||| | |||||||| || ||       |||
Db        379 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 438

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |   | ||  || ||| |||  |  |||||  | |||||
Db        439 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 498

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |     |     | |  ||| |||||  |   ||   | |    ||  |  |
Db        499 AAAAAGCTGAAATGTACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 558

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              ||| ||||||||||     ||    ||| |   | | || |||       | ||||||  |
Db        559 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 618

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db        619 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 678

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||     |   |||| ||||
Db        679 TTAGAGATTTTGGATGATACTGT 701
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RESULT 14
US-09-954-456-1131
; Sequence 1131, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1131
; LENGTH: 5189
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1131

Query Match 10.6%; Score 111; DB 9; Length 5189;
Best Local Similarity 54.1%; Pred. No. 2.4e-20;

```
  Matches  272;  Conservative    0;  Mismatches  225;  Indels    6;  Gaps    2;

Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |     |  ||| |     | | | || || || || || |||||  ||||
Db        433 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 492

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
              |  |  | |||    ||    || || |||||     | ||| | |||||   |
Db        493 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 549

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | ||| |  |  | ||  ||| |       || | | | || ||  |  |  ||
Db        550 AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 609

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  ||||| |||| | |||||||| || ||      |||
Db        610 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 669

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |   | ||  || ||| ||| |  ||||| | |||||
Db        670 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 729

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |      |      | |  ||| |||||  |   ||   | |    ||  |  |
Db        730 AAAAAGCTGAAATGTACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 789

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              ||| ||||||||||    ||   ||| |   | | || |||      | ||||||  |
Db        790 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 849

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db        850 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 909

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||    |   |||| ||||
Db        910 TTAGAGATTTTGGATGATACTGT 932


RESULT 15
US-09-292-758-31
; Sequence 31, Application US/09292758
; Publication No. US20020197602A1
; GENERAL INFORMATION:
;  APPLICANT: Burmer, Glenna C.
;  APPLICANT: Brown, Joseph P.
;  APPLICANT: LifeSpan BioSciences, Inc.
;  TITLE OF INVENTION: Nucleic Acid Sequences and Proteins
;  TITLE OF INVENTION: Associated With Aging
;  FILE REFERENCE: 017473-001110US
;  CURRENT APPLICATION NUMBER: US/09/292,758
;  CURRENT FILING DATE: 1999-04-14
;  EARLIER APPLICATION NUMBER: US 60/081,887
;  EARLIER FILING DATE: 1998-04-15
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
;   LENGTH: 5189
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-292-758-31

  Query Match             10.6%;  Score 111;  DB 9;  Length 5189;
  Best Local Similarity   54.1%;  Pred. No. 2.4e-20;
  Matches  272;  Conservative    0;  Mismatches  225;  Indels    6;  Gaps    2;

Qy        396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
              ||||  |  |     |  ||| |     | | | || || || || || |||||  ||||
Db        433 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 492

Qy        456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515
              |  |  | |||    ||    || || |||||     | ||| | |||||   |
Db        493 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG 549

Qy        516 AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
              |   | ||| |  |  | ||  ||| |       || | | | || ||  |  |  ||
Db        550 AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG 609

Qy        573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632
              |  ||||| ||  | || ||  ||||| |||| | |||||||| || ||      |||
Db        610 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 669

Qy        633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC 692
              ||| | | ||||| ||   | |   | ||  || ||| ||| |  ||||| | |||||
Db        670 CTTCTACGTGACTTTGATATCAAATTGAAGAATTTTGTGGAGTTGACAGATGTTGCCAAT 729

Qy        693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752
              ||||  |      |      | |  ||| |||||  |   ||   | |    ||  |  |
Db        730 AAAAAGCTGAAATGTACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT 789

Qy        753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812
              ||| ||||||||||    ||   ||| |   | | || |||      | ||||||  |
Db        790 AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT 849

Qy        813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872
              || | |||  ||  || ||||| || ||||||||||||    |    | |||||     |
Db        850 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 909

Qy        873 CTTAAGGACCTTCCTGATGCTGT 895
              |  ||    |   |||| ||||
Db        910 TTAGAGATTTTGGATGATACTGT 932


Search completed: July 11, 2005, 09:33:02
Job time : 5296 secs
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